

SEQUENCE LISTING

<110> Edwards, Jean-Baptiste Dumas Milne
Duclert, Aymeric
Bougueleret, Lydie

<120> Extended cDNAs for Secreted Proteins

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<150> 60/066,677

<151> 1997-11-13

<160> 227

<170> Patent.pm

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taatggtctc gtgcgaattc ttgat 25

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agggaggagg aaacagcgtg agtcc

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atgggaaagg aaaagactca tatca

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<400> 12
agcagcaaca atcaggacag cacag

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<400> 16
cacgagagag actacacggt actgg

25

<210> 17
<211> 526
<212> DNA
<213> Homo Sapiens

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aatatrarac agctacaata ttccagggcc artcacttgc cattttctcat aacagcgtca	60
gagagaaaaga actgactgar acgttttgag atg aag aaa gtt ctc ctc ctg atc	113
Met Lys Lys Val Leu Leu Leu Ile	
-15	-10
aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag	161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln	
-5	1
gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr	209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly	
10	15
wtg ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att	257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile	
25	30
cca ttt cca aga ttt cca tgg ttt aga cgt aan ttt cct att cca ata	305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile	
40	45
cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa	354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys	
60	65
ggaaaaagtc crataaacct gggtcacctga aattgaaatt gagccacttc cttgaaraat	414
caaaatttcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta	474
gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aa	526

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<220>
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 <222> 1..17
 <223> Von Heijne matrix
 score 8.2
 seq LLLITAILAVAVG/FP

<400> 18

Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
1 5 10 15
Gly

<210> 19
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 <212> DNA
 <213> Homo Sapiens

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 <223> blastn

<221> misc_feature
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 <222> 61..399
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<221> misc_feature
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<221> misc_feature
 <222> 60..399
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<221> misc_feature
 <222> 393..432
 <223> blastn

<221> sig_peptide
 <222> 346..408
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 ctgatgccga gttccgtctc tcgcgtcttt tcctgggtccc aggcaaagcg gasgnagatc 120
 ctcaaacggc ctagtgcttc gcgcttccgg agaaaatcag cggctctaatt aattcctctg 180
 gtttgttgaa gcagttacca agaattcttca accctttccc acaaaagcta attgagtaca 240
 cgttcctggt gagtacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg 300
 aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt 357
 Met Trp Trp Phe
 -20
 cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct 405
 Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
 -15 -10 -5
 gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata 453
 Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile

1	5	10	15	
gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca raa				501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa				
	20	25	30	
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgt caa				549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln				
	35	40	45	
aaa tagaaatcag gaarataatt caacttaaag aakttcattt catgaccaaa				602
Lys				
ctcttcaraa acatgtcttt acaagcatat ctcttgattt gctttctaca ctgttgaatt				662
gtctggcaat atttctgcag tggaaaattt gatttarmta gttcttgact gataaatatg				722
gtaaggtggg cttttccccc tgtgtaattg gctactatgt cttactgagc caagttgtaw				782
tttgaaataa aatgatatga gagtgacaca aaaaaaaaaa				822

<210> 20
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 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> 1..21
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 score 5.5
 seq SFLPSALVIWTS/AF

<400> 20
 Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
 1 5 10 15
 Ile Trp Thr Ser Ala
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<210> 21
 <211> 405
 <212> DNA
 <213> Homo Sapiens

<220>
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<221> sig_peptide
 <222> 185..295
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<400> 21	
atcaccttct tctccatcct tstctgggcc agtccccarc ccagtccctc tcttgacctg	60
cccagcccaa gtcagccttc agcacgcgct tttctgcaca cagatattcc aggcctacct	120
ggcattccag gacctccgma atgatgtctc agtcccttac aagcgccttc tggatgaggg	180
tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg	229
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val	
-35 -30 -25	
aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc	277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala	
-20 -15 -10	

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ctg tcc ccc tgt ctg acc gct cca aak tcc ccc cgg ctt gct atg atg      325
Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Arg Leu Ala Met Met
    -5              1              5              10
cct gac aac taaatatacct tatccaaatc aataaarwra raatcctccc      374
Pro Asp Asn
tccaraaggg tttctaaaaa caaaaaaaaaa a      405

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<210> 22
<211> 37
<212> PRT
<213> Homo Sapiens

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<220>
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<222> 1..37
<223> Von Heijne matrix
      score 5.9
      seq LSYASSALSPCLT/AP

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<400> 22
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
1              5              10              15
Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
      20              25              30
Ser Pro Cys Leu Thr
      35

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<210> 23
<211> 496
<212> DNA
<213> Homo Sapiens

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<220>
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<223> blastn

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<223> blastn

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<221> sig_peptide
<222> 196..240
<223> Von Heijne matrix

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<400> 23
aaaaaattgg tcccagtttt caccctgccg cagggctggc tggggagggc agcggtttag      60
attagccgtg gcctaggccg tttaacgggg tgacacgagc ntgcagggcc gagtccaagg      120
cccggagata ggaccaaccg tcaggaatgc gaggaatggt tttcttcgga ctctatcgag      180
gcacacagac agacc atg ggg att ctg tct aca gtg aca gcc tta aca ttt      231
          Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
          -15              -10              -5

```



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gcc ara gcc ctg gac ggc tgc aga aat ggc att gcc cac cct gca agt      279
Ala Xaa Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
      1          5          10
gag aag cac aga ctc gag aaa tgt agg gaa ctc gag asc asc cac tcg      327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Xaa Xaa His Ser
      15          20          25
gcc cca gga tca acc cas cac cga aga aaa aca acc aga aga aat tat      375
Ala Pro Gly Ser Thr Xaa His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
      30          35          40          45
tct tca gcc tgaaatgaak ccgggatcaa atggttgctg atcaragccc      424
Ser Ser Ala
atattttaat tggaaaagtc aaattgasca ttattaaata aagcttgttt aatatgtctc      484
aaacaaaaaa aa      496

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<210> 24
<211> 15
<212> PRT
<213> Homo Sapiens

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<220>
<221> SIGNAL
<222> 1..15
<223> Von Heijne matrix
      score 5.5
      seq ILSTVTALTFAXA/LD

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<400> 24
Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Xaa Ala
      1          5          10          15

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<210> 25
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<212> DNA
<213> Homo Sapiens

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<221> sig_peptide
<222> 49..96
<223> Von Heijne matrix

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aaagatccct gcagcccggc aggagagaag gctgagcctt ctggcgtc atg gag agg      57
                                     Met Glu Arg
                                     -15
ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc      105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
      -10          -5          1
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag      153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
      5          10          15
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac      201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
      20          25          30          35
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt aaa tgg agt gta      249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
      40          45          50

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cgc gtc ctg ctc agc aaa cgc tgt gct ccc aga tgt ccc aac gac aac	297
Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn	
55 60 65	
atg aak ttc gaa tgg tcg ccg gcc ccc atg gtg caa ggc gtg atc acc	345
Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr	
70 75 80	
agg cgc tgc tgt tcc tgg gct ctc tgc aac agg gca ctg acc cca cag	393
Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln	
85 90 95	
gag ggg cgc tgg gcc ctg cra ggg ggg ctc ctg ctc cag gac cct tcg	441
Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser	
100 105 110 115	
agg ggc ara aaa acc tgg gtg cgg cca cag ctg ggg ctc cca ctc tgc	489
Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys	
120 125 130	
ctt ccc awt tcc aac ccc ctc tgc cca rgg gaa acc cag gaa gga	534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly	
135 140 145	
taacactgtg ggtgccccca cctgtgcatt gggaccacra cttcaccctc ttggaracaa	594
taaactctca tgcccccaaaa aaaaaaaaaa	623

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<210> 26
<211> 16
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<213> Homo Sapiens

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Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala
1          5          10          15

<210> 27
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<212> DNA
<213> Homo Sapiens

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<221> sig_peptide
<222> 32..73
<223> Von Heijne matrix

<400> 27
aactttgcct tgtgttttcc accctgaaag a atg ttg tgg ctg ctc ttt ttt          52
                        Met Leu Trp Leu Leu Phe Phe
                        -10

ctg gtg act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat          100
Leu Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn
-5          1          5

gct ttt aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca          148
Ala Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala

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10		15		20		25	
tat gcc tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct							196
Tyr Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala							
	30		35		40		
ttc tcc atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat							244
Phe Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His							
	45		50		55		
gtc cta ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt							292
Val Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val							
	60		65		70		
aca gac cct tca aaa aat cac acc ctt cct gct gtt gag gtg caa tca							340
Thr Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser							
	75		80		85		
gcc ata aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat							388
Ala Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn							
	90		95		100		105
gac caa act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc							436
Asp Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro							
	110		115		120		
atg gac cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt							484
Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe							
	125		130		135		
tgc atc atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg							532
Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp							
	140		145		150		
caa cgt ada ara aag aac aaa gaa cca tct gaa gtg gat gac gct gaa							580
Gln Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu							
	155		160		165		
rat aak tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat							628
Xaa Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp							
	170		175		180		185
ccc ctg gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag							676
Pro Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu							
	190		195		200		
gat gag agg ctc acc cct ctc tgaagggtg ttgttctgct tcctcaaraa							727
Asp Glu Arg Leu Thr Pro Leu							
	205						
attaaacatt tgtttctgtg tgactgctga gcatcctgaa ataccaagag cagatcatat							787
wttttgtttc accattcttc ttttgtaata aattttgaat gtgcttgaaa aaaaaaaaaa							847
c							848

<210> 28

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<222> 1..14

<223> Von Heijne matrix

score 10.7

seq LWLLFFLVTAIHA/EL

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1

5

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<210> 29
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<220>
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<400> 29
gggaagatgg agatagtatt gcctg

25

<210> 30
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
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<400> 30
ctgccatgta catgatagag agattc

26

<210> 31
<211> 546
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<220>
<221> promoter
<222> 1..517

<221> transcription start site
<222> 518

<221> protein_bind
<222> 17..25
<223> matinspector prediction
name CMYB_01
score 0.983
sequence tgtcagttg

<221> protein_bind
<222> complement(18..27)
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name MYOD_Q6
score 0.961
sequence cccaactgac

<221> protein_bind
<222> complement(75..85)
<223> matinspector prediction
name S8_01
score 0.960
sequence aatagaattag

<221> protein_bind
<222> 94..104
<223> matinspector prediction
name S8_01
score 0.966
sequence aactaaattag

<221> protein_bind
<222> complement(129..139)
<223> matinspector prediction
name DELTAEF1_01
score 0.960
sequence gcacacctcag

<221> protein_bind
<222> complement(155..165)
<223> matinspector prediction
name GATA_C
score 0.964
sequence agataaatcca

<221> protein_bind
<222> 170..178
<223> matinspector prediction
name CMYB_01
score 0.958
sequence cttcagttg

<221> protein_bind
<222> 176..189
<223> matinspector prediction
name GATA1_02
score 0.959
sequence ttgtagataggaca

<221> protein_bind
<222> 180..190
<223> matinspector prediction
name GATA_C
score 0.953
sequence agataggacat

<221> protein_bind
<222> 284..299
<223> matinspector prediction
name TAL1ALPHA47_01
score 0.973
sequence cataacagatggtaag

<221> protein_bind
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name TAL1BETA47_01
score 0.983
sequence cataacagatggtaag

<221> protein_bind
<222> 284..299

<223> matinspector prediction
name TAL1BETAITF2_01
score 0.978
sequence cataacagatggtaag

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<223> matinspector prediction
name MYOD_Q6
score 0.954
sequence accatctgtt

<221> protein_bind
<222> complement(302..314)
<223> matinspector prediction
name GATA1_04
score 0.953
sequence tcaagataaagta

<221> protein_bind
<222> 393..405
<223> matinspector prediction
name IK1_01
score 0.963
sequence agttgggaattcc

<221> protein_bind
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<223> matinspector prediction
name IK2_01
score 0.985
sequence agttgggaattc

<221> protein_bind
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<223> matinspector prediction
name CREL_01
score 0.962
sequence tgggaattcc

<221> protein_bind
<222> 423..436
<223> matinspector prediction
name GATA1_02
score 0.950
sequence tcagtgatatggca

<221> protein_bind
<222> complement(478..489)
<223> matinspector prediction
name SRY_02
score 0.951
sequence taaaacaaaaca

<221> protein_bind
<222> 486..493
<223> matinspector prediction
name E2F_02

score 0.957
sequence tttagcgc

<221> protein_bind
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name MZF1_01
score 0.975
sequence tgagggga

<400> 31
tgagtgcagt gttacatgtc agttggggtta agtttggttaa tgtcattcaa atcttctatg 60
tcttgatttg cctgctaatt ctattatttc tggaaactaaa ttagtttgat ggttctatta 120
gttattgact gaggtgtgct aatctcccat tatgtggatt tatctatttc ttcagttgta 180
gataggacat tgatagatac ataagtacca ggacaaaagc agggagatct tttttccaaa 240
atcaggagaa aaaaatgaca tctggaaaac ctatagggaa aggcataaca gatggtaagg 300
atactttatc ttgagtagga gagccttcct gtggcaacgt ggagaaggga agaggtcgta 360
gaattgagga gtcagctcag ttagaagcag ggagttggga attccgttca tgtgatttag 420
catcagtgat atggcaaagtg tgggactaag ggtagtgatc agagggttaa aattgtgtgt 480
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cttcat 546

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<211> 23
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<220>
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<400> 32
gtaccaggga ctgtgaccat tgc 23

<210> 33
<211> 24
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<213> Artificial Sequence

<220>
<221> Oligonucleotide

<400> 33
ctgtgaccat tgctcccaag agag 24

<210> 34
<211> 861
<212> DNA
<213> Homo Sapiens

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<222> 1..806

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<222> 807

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name NFY_Q6
score 0.956
sequence ggaccaatcat

<221> protein_bind
<222> 70..77
<223> matinspector prediction
name MZF1_01
score 0.962
sequence cctgggga

<221> protein_bind
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<223> matinspector prediction
name CMYB_01
score 0.994
sequence tgaccgttg

<221> protein_bind
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name VMYB_02
score 0.985
sequence tccaacggt

<221> protein_bind
<222> 135..143
<223> matinspector prediction
name STAT_01
score 0.968
sequence ttcctggaa

<221> protein_bind
<222> complement(135..143)
<223> matinspector prediction
name STAT_01
score 0.951
sequence ttccaggaa

<221> protein_bind
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name MZF1_01
score 0.956
sequence ttggggga

<221> protein_bind
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name IK2_01
score 0.965
sequence gaatgggatttc

<221> protein_bind
<222> 384..391

<223> matinspector prediction
 name MZF1_01
 score 0.986
 sequence agagggga

<221> protein_bind
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 name SRY_02
 score 0.955
 sequence gaaaacaaaaca

<221> protein_bind
 <222> 592..599
 <223> matinspector prediction
 name MZF1_01
 score 0.960
 sequence gaagggga

<221> protein_bind
 <222> 618..627
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 name MYOD_Q6
 score 0.981
 sequence agcatctgcc

<221> protein_bind
 <222> 632..642
 <223> matinspector prediction
 name DELTAEF1_01
 score 0.958
 sequence tcccaccttc

<221> protein_bind
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 <223> matinspector prediction
 name S8_01
 score 0.992
 sequence gaggaattat

<221> protein_bind
 <222> complement(824..831)
 <223> matinspector prediction
 name MZF1_01
 score 0.986
 sequence agagggga

<400> 34
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 cggtgaccgt tggattcctg gaagcagtag ctgttctgtt tggatctggg agggacaggg 180
 ctacagagggc taggcacgag ggaaggctcag aggagaaggs aggsarggcc cagtgagarg 240
 ggagcatgcc ttcccccaac cctggcttsc ycttggymam agggcgkttt tgggmacttr 300
 aaytcagggc ccaascagaa scacaggccc aktcntggct smaagcacia tagcctgaat 360
 gggatttcag gttagnacagg gtgagagggg aggcctctctg gcttagtttt gttttgtttt 420
 ccaaatacaag gtaacttgct cccttctgct acgggccttg gtcttggtt gtcctcacc 480
 agtcggaact ccctaccact ttcaggagag tggttttagg cccgtggggc tgttctgttc 540
 caagcagtgt gagaacatgg ctggtagagg ctctagctgt gtgcggggcc tgaaggggag 600

tgggttctcg	cccaaagagc	atctgcccat	ttcccacctt	cccttctccc	accagaagct	660
tgccctgagct	gtttggacaa	aaatccaaac	cccacttggc	tactctggcc	tggttcagc	720
ttggaaccca	atacctaggc	ttacaggcca	tcctgagcca	ggggcctctg	gaaattctct	780
tcctgatggt	cctttagggt	tgggcacaaa	atataattgc	ctctcccctc	tcccattttc	840
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<400> 35
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<210> 36
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<220>
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<400> 36
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<210> 37
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 name ARNT_01
 score 0.964
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<221> protein_bind
 <222> 193..204
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 name NMYC_01
 score 0.965
 sequence actcacgtgctg

<221> protein_bind

<222> 193..204
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name USF_01
score 0.985
sequence actcacgtgctg

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name USF_01
score 0.985
sequence cagcacgtgagt

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
name NMYC_01
score 0.956
sequence cagcacgtgagt

<221> protein_bind
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name MYCMAX_02
score 0.972
sequence cagcacgtgagt

<221> protein_bind
<222> 195..202
<223> matinspector prediction
name USF_C
score 0.997
sequence tcacgtgc

<221> protein_bind
<222> complement(195..202)
<223> matinspector prediction
name USF_C
score 0.991
sequence gcacgtga

<221> protein_bind
<222> complement(210..217)
<223> matinspector prediction
name MZF1_01
score 0.968
sequence catgggga

<221> protein_bind
<222> 397..410
<223> matinspector prediction
name ELK1_02
score 0.963
sequence ctctccggaagcct

<221> protein_bind
<222> 400..409
<223> matinspector prediction

name CETS1P54_01
score 0.974
sequence tccggaagcc

<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
name AP1_Q4
score 0.963
sequence agtgactgaac

<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
name AP1FJ_Q2
score 0.961
sequence agtgactgaac

<221> protein_bind
<222> 547..555
<223> matinspector prediction
name PADS_C
score 1.000
sequence tgtggtctc

<400> 37

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kawaagctca	gcaccggtgc	ccatcacagg	gccggcagca	cacacatccc	attactcaga	180
aggaactgac	ggactcacgt	gctgctccgt	ccccatgagc	tcagtggacc	tgtctatgta	240
gagcagtcag	acagtgcctg	ggatagagtg	agagttcagc	cagtaaatcc	aagtgattgt	300
cattcctgtc	tgcattagta	actcccaacc	tagatgtgaa	aacttagttc	tttctcatag	360
gttgctctgc	ccatgggtccc	actgcagacc	caggcactct	ccggaagcct	ggaaatcacc	420
cggtgtctct	gcctgtctccc	gtcacatccc	cacacttgtg	ttcagtcact	gagttacaga	480
ttttgcctcc	tcaatttctc	ttgtcttagt	cccatcctct	gttcccctgg	ccagtttgtc	540
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<210> 38

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<221> Oligonucleotide

<400> 38

ggccatacac ttgagtgac

19

<210> 39

<211> 19

<212> DNA

<213> Artificial Sequence

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<221> Oligonucleotide

<400> 39
atatagacaa acgcacacc

19

<210> 40
<211> 1098
<212> DNA
<213> Homo sapiens

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<222> 173..211
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<221> polyA_signal
<222> 1063..1068

<221> polyA_site
<222> 1087..1098

<221> misc_feature
<222> 144..467
<223> homology
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<221> misc_feature
<222> 510..640
<223> homology
id :AA057573
est

<221> misc_feature
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<223> homology
id :AA057573
est

<221> misc_feature
<222> 708..786
<223> homology
id :AA057573
est

<221> misc_feature
<222> 635..682
<223> homology
id :AA057573
est

<221> misc_feature
<222> 625..1084
<223> homology
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<221> misc_feature
<222> 779..1084
<223> homology
id :R71351
est

<221> misc_feature
<222> 144..506
<223> homology
id :H12619
est

<221> misc_feature
<222> 90..467
<223> homology
id :T03538
est

<221> misc_feature
<222> 314..523
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id :T34150
est

<221> misc_feature
<222> 567..687
<223> homology
id :T34150
est

<221> misc_feature
<222> 686..730
<223> homology
id :T34150
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<221> misc_feature
<222> 510..553
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<221> misc_feature
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est

<221> misc_feature
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est

<221> misc_feature
<222> 510..553
<223> homology
id :N32314

est

<221> misc_feature
<222> 352..523
<223> homology
id :T77966
est

<221> misc_feature
<222> 218..351
<223> homology
id :T77966
est

<221> misc_feature
<222> 510..553
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<221> misc_feature
<222> 550..917
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id :AA464128
est

<400> 40

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Cgacagcgcc ggcccctgcg gcccgcaagt cgtcacagac gatgatggcc agggcccggg      120
ggctaaggac ggcagctcct ttagcggcag agttttccga gtgaccttct tg atg ctg      178
                                         Met Leu
gct gtt tct ctc acc gtt ccc ctg ctt gga gcc atg atg ctg ctg gaa      226
Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu Leu Glu
-10 -5 1 5
tct cct ata gat cca cag cct ctc agc ttc aaa gaa ccc ccg ctc ttg      274
Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro Leu Leu
10 15 20
ctt ggt gtt ctg cat cca aat acg aag ctg cga cag gca gaa agg ctg      322
Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu Arg Leu
25 30 35
ttt gaa aat caa ctt gtt gga cgg gag tcc ata gca cat att ggg gat      370
Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile Gly Asp
40 45 50
gtg atg ttt act ggg aca gca gat ggc cgg gtc gta aaa ctt gaa aat      418
Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu Glu Asn
55 60 65
ggt gaa ata gag acc att gcc cgg ttt ggt tcg ggc cct tgc aaa acc      466
Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys Lys Thr
70 75 80 85
cga ggt gat gag cct gtg tgt ggg aga ccc ctg ggt atc cgt ggc agg      514
Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg Gly Arg
90 95 100
gcc caa tgg gac tct ctt tgt ggc cga tgc ata caa agg gac tat ttg      562
Ala Gln Trp Asp Ser Leu Cys Gly Arg Cys Ile Gln Arg Asp Tyr Leu
105 110 115
aag taaatccctg gaaacgtgaa gtgaaactgc tgctgtcctc cgagacaccc      615
Lys
attgaggggga agaacatgtc ctttgtgaat gatcttacag tcactcagga tgggaggaag      675
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<210> 41
<211> 855
<212> DNA
<213> Homo sapiens
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<222> 817..822
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<221> polyA_site
<222> 842..855
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<221> misc_feature
<222> 608..811
<223> homology
      id :M85769
      est
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24

cagagaagaa catttaaagg gttaatatTT ttgaaacgtt ttcagataat atctatttga	785
ttattgtggc ttctatttga aatgtgtcta aaataaaatg ctgtttattt aaaatgaaaa	845
aaaaaaaaaa	855

<210> 42
 <211> 1176
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 174..266
 <223> Von Heijne matrix
 score 3.5
 seq WSPLSTRSGGTHA/CS

<221> polyA_signal
 <222> 1144..1149

<221> polyA_site
 <222> 1165..1176

<221> misc_feature
 <222> 886..1134
 <223> homology
 id :AA595193
 est

<221> misc_feature
 <222> 756..894
 <223> homology
 id :AA595193
 est

<221> misc_feature
 <222> 655..755
 <223> homology
 id :AA595193
 est

<221> misc_feature
 <222> 167..367
 <223> homology
 id :W81213
 est

<221> misc_feature
 <222> 66..172
 <223> homology
 id :W81213
 est

<221> misc_feature
 <222> 429..508
 <223> homology
 id :W81213
 est

<221> misc_feature
<222> 756..894
<223> homology
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est

<221> misc_feature
<222> 536..643
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<223> homology
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<221> misc_feature
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<221> misc_feature
<222> 655..755
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<222> 756..847
<223> homology

id :AA179182
est

<221> misc_feature
<222> 3..338
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<221> misc_feature
<222> 334..374
<223> homology
id :HUM524F05B
est

<221> misc_feature
<222> 886..1134
<223> homology
id :AA398156
est

<221> misc_feature
<222> 756..894
<223> homology
id :AA398156
est

<400> 42

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tggcgcgtgg	actccgctgc	ctcccccatc	tccccgccat	ctgcgcccgg	agg atg	176
					Met	
agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc tcc						224
Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Ser						
-30	-25		-20		-15	
ttc tgg agc cct ttg tcc acc agg tcg ggg ggc act cat gcg tgc tcc						272
Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys Ser						
	-10		-5		1	
gct tca atg aga caa ccc tgg gca agc ccc tgg tcc caa ggg aac atc						320
Ala Ser Met Arg Gln Pro Trp Ala Ser Pro Trp Ser Gln Gly Asn Ile						
5	10		15			
agt tct acg aga ccc tcc ctg ctg aga tgc gca aat tct ctc ccc agt						368
Ser Ser Thr Arg Pro Ser Leu Leu Arg Cys Ala Asn Ser Leu Pro Ser						
20	25		30			
aca aag gac aaa gcc aaa ggc ccc ttg tta gct ggc cat ccc tgc ccc						416
Thr Lys Asp Lys Ala Lys Gly Pro Leu Leu Ala Gly His Pro Cys Pro						
35	40		45		50	
att ttt tcc cct ggt cct ttc ccc tgt ggc cac agg gaa gtg tgg cct						464
Ile Phe Ser Pro Gly Pro Phe Pro Cys Gly His Arg Glu Val Trp Pro						
	55		60		65	
gaa tac ccc acc ccg gct cct ctg cac cca gag ctg ggg gcc acc tca						512
Glu Tyr Pro Thr Pro Ala Pro Leu His Pro Glu Leu Gly Ala Thr Ser						
	70		75		80	
gaa gtg tca tct ctc tct gag cac gsa ttc ccc tgc agc agt cga gga						560
Glu Val Ser Ser Leu Ser Glu His Xaa Phe Pro Cys Ser Ser Arg Gly						
85	90		95			
ctg agc aga ttg agt gat gct ggg gca gan adg cct gag ang aaa ggt						608
Leu Ser Arg Leu Ser Asp Ala Gly Ala Xaa Xaa Pro Glu Xaa Lys Gly						

100	105	110	
ggt cag cca gtc gtt tgt aag gcg ctc gkc ggm act gct gaa acg ccc			656
Val Gln Pro Val Val Cys Lys Ala Leu Xaa Gly Thr Ala Glu Thr Pro			
115	120	125	130
cca ccc tgacagcccc atcctcaaag actgtcttaa ttactcatgg caggttctag			712
Pro Pro			
agacttaagg ggaaaagctg ctttcaaggc caccacatgt ctggtgctcc ccmaccagst			772
statctgcct wgtgttcatt ttgytatttt gtgasgtgag acagcaaaga ccaataaaaa			832
catattttat aagaacaaaa ggcytgggtg cctaccgkg tgggggcacw gtgggaagcc			892
ttctgmtagg gtgtcttggtg ctgtrtgggtg tgttttggtt gccccyttat ttgctttgc			952
ttaccagtc ttcccytamt yttggatgst tyttaaccct caggcaaacc tgtgttcccc			1012
ctgtattcag gstytgcttt aaagcaagcc atgaggctgt tggagtttct gtttagggca			1072
ttaaaaattc ccgcaaacta taaagagcaa tgttttcagt yttttaggat tagaagaatt			1132
acataaaaat taataaacat tttcaatgat ggaaaaaaaaaaaa			1176

<210> 43
 <211> 648
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 460..555
 <223> Von Heijne matrix
 score 4
 seq FSFMLLGMGGLP/GF

<221> polyA_signal
 <222> 614..619

<221> polyA_site
 <222> 635..648

<400> 43
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 tccttagagt tctccctcca ttagtagttg tcttagggtc tgtttctggg gagccctgcc 120
 taagactcat gctacaagaa gttaaataag tttcccgaag tcacacagct agcctctcat 180
 cccttttcta ctgagaggaa gtggaatgca ctccgacaag gataagggtt tattgtgagc 240
 tggccttgga attaaaccac caccaacaca cttttggatt atcagaaggt ggaaggagtg 300
 caaatgccag ttacggtgat gcgttcaaca tccttatttc cagtctttat gacgcctttc 360
 ctgaatcaca ggtgcattgg ggtgcttcc cctccccagg actccacccc aactttgtga 420
 acacaacca cttagaggag ttatctcagc acattatga atg ttg ggg acc acg 474
 Met Leu Gly Thr Thr
 -30

ggc ctc ggg aca cag ggt cct tcc cag cag gct ctg ggc ttt ttc tcc 522
 Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala Leu Gly Phe Phe Ser
 -25 -20 -15
 ttt atg tta ctt gga atg ggc ggg tgc ctg cct gga ttc ctg cta cag 570
 Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro Gly Phe Leu Leu Gln
 -10 -5 1 5
 cct ccc aat cga tct cct act ttg cct gca tcc acc ttt gcc cat 615
 Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser Thr Phe Ala His
 10 15 20
 taaagtcaat tctccacca taaaaaaaaaaa aaa 648

<210> 44

<211> 1251
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> sig_peptide
 <222> 79..369
 <223> Von Heijne matrix
 score 4
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<221> polyA_signal
 <222> 1217..1222

<221> polyA_site
 <222> 1240..1251

<221> misc_feature
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 <223> homology
 id :AA056667
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<221> misc_feature
 <222> 463..520
 <223> homology
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
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<223> homology
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
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id :AA595195
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<221> misc_feature
<222> 1208..1237
<223> homology
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<221> misc_feature
<222> 223..522
<223> homology
id :AA041216
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<221> misc_feature
<222> 518..636
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id :AA041216
est

<221> misc_feature
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id :N94607
est

<221> misc_feature
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id :N94607
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<221> misc_feature
<222> 833..1195
<223> homology
id :AA076410
est

<400> 44

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gagagaaggg	ggttcatac	atg gcg gat gac cta aag cga ttc ttg tat aaa				111
		Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys				
		-95		-90		
aag tta cca agt gtt gaa ggg ctc cat gcc att gtt gtg tca gat aga						159
Lys Leu Pro Ser Val Glu Gly Leu His Ala Ile Val Val Ser Asp Arg						
-85		-80		-75		
gat gga gta cct gtt att aaa gtg gca aat gac aat gct cca gag cat						207
Asp Gly Val Pro Val Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His						
-70		-65		-60		-55
gct ttg cga cct ggt ttc tta tcc act ttt gcc ctt gca aca gac caa						255
Ala Leu Arg Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln						
		-50		-45		-40
gga agc aaa ctt gga ctt tcc aaa aat aaa agt atc atc tgt tac tat						303
Gly Ser Lys Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr						
-35		-30				-25
aac acc tac cag gtg gtt caa ttt aat cgt tta cct ttg gtg gtg agt						351
Asn Thr Tyr Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser						
-20		-15		-10		
ttc ata gcc agc agc agt gcc aat aca gga cta att gtc agc cta gaa						399
Phe Ile Ala Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu						
-5		1		5		10
aag gag ctt gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa att						447
Lys Glu Leu Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Ile						
		15		20		25
tct taatctgaca gtggtttcag tgtgtacctt atcttcatta taacaacaca						500
Ser						
atatcaatcc agcaatcttt agactacaat aatgctttta tccatgtgct caagaaaggg						560
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atggttcagt ctatcacagc tcccatggag ttagtctggt caccagatat ggatgagaga						740
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ccaattgtac aatatgccca ggcttgacaga ataaagccaa ctttttattg tgaataataa						860
taaggacata tttttcttca gattatgttt tatttctttg cattgagtga ggtacataaa						920
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ttgcagtata gatgaatatt actaatcagt ttgattattc tcagaggggtg ctgctcttta						1040

atgaaaatga aaattatagc taatgttttt tcctcaaact ctgctttctg taaccaatca	1100
gtgttttaaat gtttggtgtgt tcttcataaa atttaaatac aattcggtat tctgtttcca	1160
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ggagcagtcct ctgaagacgc ttctactgag aggtctgcc atg gcc tct ctt ggc      174
                               Met Ala Ser Leu Gly
                               -20
ctc caa ctt gtg ggc tac atc cta ggc ctt ctg ggg ctt ttg ggc aca      222
Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu Gly Leu Leu Gly Thr
                               -15                               -10                               -5
ctg gtt gcc atg ctg ctc ccc agc tgg aaa aca agt tct tat gtc ggt      270
Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr Ser Ser Tyr Val Gly
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gcc agc att gtg aca gca gtt ggc ttc tcc aag ggc ctc tgg atg gaa      318
Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys Gly Leu Trp Met Glu
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tgt gcc aca cac agc aca ggc atc acc cag tgt gac atc tat agc acc      366
Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys Asp Ile Tyr Ser Thr
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ctt ctg ggc ctg ccc gct gac atc cak gct gcc cag gcc atg atg gtg      414
Leu Leu Gly Leu Pro Ala Asp Ile Xaa Ala Ala Gln Ala Met Met Val
                               50                               55                               60
aca tcc agt gca atc tcc tcc ctg gcc tgc att atc tct gtg gtg ggc      462
Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly
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atg ara tgc aca gtc ttc tgc cag gaa tcc cga gcc aaa gac aga gtg      510
Met Xaa Cys Thr Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val
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gcg gta gca ggt gga gtc ttt ttc atc ctt gga ggc ctc ctg gga ttc      558
Ala Val Ala Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe
                               95                               100                               105
att cct gtt gcc tgg aat ctt cat ggg atc cta cgg gac ttc tac tca      606
Ile Pro Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser
                               110                               115                               120                               125
cca ctg gtg cct gac agc atg aaa ttt gag att gga gag gct ctt tac      654
Pro Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr
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ttg ggc att att tct tcc ctg ttc tcc ctg ata gct gga atc atc ctc      702
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile Leu
                               145                               150                               155
tgc ttt tcc tgc tca tcc cag aga aat cgc tcc aac tac tac gat gcc      750
Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr Asp Ala
                               160                               165                               170
tac caa gcc caa cct ctt gcc aca agg agc tct cca agg cct ggt caa      798
Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg Pro Gly Gln
                               175                               180                               185
cct ccc aaa gtc aag agt gag ttc aat tcc tac agc ctg aca ggg tat      846
Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser Leu Thr Gly Tyr
                               190                               195                               200                               205
gtg tgaagaacca ggggccagag ctggggggtg gctgggtctg tgaaaaacag      899
Val
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tggacagcac	cccgagggcc	acaggtgagg	gacactacca	ctggatcgtg	tcagaaggtg	959
ctgctgaggg	tagactgact	ttggccattg	gattgagcaa	aggcagaaat	gggggctagt	1019
gtaacagcat	gcaggttgaa	ttgccaagga	tgctcgccat	gccagccttt	ctgttttcct	1079
caccttgctg	ctcccctgcc	ctaagtcccc	aaccctcaac	ttgaaacccc	attcccttaa	1139
gccaggamtc	agaggatccc	tytgccctck	ggtttamctg	ggactccatc	cccaaaccga	1199
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gstyttagct	cattgctggg	gatgggaagg	agaagcagtg	gctttystgg	gcattgctyt	1319
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yttgttatga	ctccacagtg	tccagamtaa	tttgtgcatg	aactgaaata	aaaccatcct	1439
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							Met Phe Ala Pro		
							-30		
gcg gtg	atg cgt	gct ttt	cgc aag	aac aag	act ctc	ggc tat	gga gtc	165	
Ala Val	Met Arg	Ala Phe	Arg Lys	Asn Lys	Thr Leu	Gly Tyr	Gly Val		
	-25			-20		-15			
ccc atg	ttg ttg	ctg att	ggt gga	ggt tct	ttt ggt	ctt cgt	gag ttt	213	
Pro Met	Leu Leu	Leu Ile	Val Gly	Gly Ser	Phe Gly	Leu Arg	Glu Phe		
	-10		-5		1				
tct caa	atc cga	tat gat	gct gtg	aag agt	aaa atg	gat cct	gag ctt	261	
Ser Gln	Ile Arg	Tyr Asp	Ala Val	Lys Ser	Lys Met	Asp Pro	Glu Leu		
5		10		15		20			
gaa aaa	aaa ccg	aaa gag	aat aaa	ata tct	tta gag	tcg gaa	tat gag	309	
Glu Lys	Lys Pro	Lys Glu	Asn Lys	Ile Ser	Leu Glu	Ser Glu	Tyr Glu		
	25		30		35				
gga agt	atc tgt	tgaagg	gcta ctatc	tttcc ttggc	cttc tccct	ttgtg		361	
Gly Ser	Ile Cys								
	40								
ggactca	aatc tccag	actat ctccc	agag aatctt	gtca aggtt	ggct ttaag	ctttg		421	
ttgggaa	aat caaag	actcc aagttt	gatg actgga	agaa tattc	gagga cccagg	cctt		481	
gggaaga	tcc tgacct	cctc caagga	agaa atccag	gaaa gcctta	agac taagaca	act		541	

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 aaaaaaaaaa 610

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caggtcattt ggagaacaag tgctttagta gtagtttaaa gtagtaactg ctactgtatt	300
tagtgggggtg gaattcagaa gaaatttgaa gaccagatca tgggtggtct gcatgtga	358
atg aac ach ttt gag cca gac agc ctg gct gtc att gct ttc ttc ctc	406
Met Asn Thr Phe Glu Pro Asp Ser Leu Ala Val Ile Ala Phe Phe Leu	
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ccc att tgg acc ttc tct gcc ctt aca ttt ttg ttt ctc cat cta cca	454
Pro Ile Trp Thr Phe Ser Ala Leu Thr Phe Leu Phe Leu His Leu Pro	
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cct ctt ggc ttg att ttg ctt ctt tct ttc tgt gga gga tat act aag	550
Pro Leu Gly Leu Ile Leu Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys	
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Cys Asp Phe Ala Leu Ser Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe	
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tct att atg gat cca aaa aga aaa aca aaa tgc taatgaagcc atcasgtcaa	651
Ser Ile Met Asp Pro Lys Arg Lys Thr Lys Cys	
45 50 55	
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gtgagctgct gagatttggg agtctgcgct aggcccgctt ggagttctga gccgatggaa      180
gagttcactc atg ttt gca ccc gcg gtg atg cgt gct ttt cgc aag aac      229
          Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn
          -30                      -25                      -20
aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg att gtt gga ggt      277
Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly
          -15                      -10                      -5
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Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys
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Gly Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile
          15                      20                      25
tct tta gag tcg gaa tat gag aaa atc aaa gac tcc aag ttt gat gac      421
Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp
          30                      35                      40                      45
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Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu
          50                      55                      60
caa gga aga aat cca gaa agc ctt aag act aag aca act tgactctgct      518
Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
          65                      70
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acttctatca agtggaaagg aaattccagg cccatggaaa cttggatatg ggtaatttgg      638
atggacaaaa ktaatctktc actaaaggtc atgtaccagg tttttatact tcccagctaa      698
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<221> misc_feature
<222> 410..439
<223> homology
      id :H04537
      est

<221> misc_feature
<222> 572..687
<223> homology
      id :AA466632
      est

<221> misc_feature
<222> 260..444
<223> homology
      id :AA459511
      est

<221> misc_feature
<222> 449..567
<223> homology
      id :AA459511
      est

<221> misc_feature
<222> 117..184
<223> homology
      id :AA459511
      est

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<221> misc_feature
 <222> 260..464
 <223> homology
 id :H57434
 est

<221> misc_feature
 <222> 118..184
 <223> homology
 id :H57434
 est

<221> misc_feature
 <222> 56..113
 <223> homology
 id :H57434
 est

<221> misc_feature
 <222> 454..485
 <223> homology
 id :H57434
 est

<400> 49

actcctttta	gcataggggc	ttcggcgcca	gcggccagcg	ctagtcgggc	tggttaagtgc	60
ctgatgccga	gttccgtctc	tcgcgtcttt	tcctggtccc	aggcaaagcg	gasgnagatc	120
ctcaaacggc	ctagtgtctc	gcgcttccgg	agaaaatcag	cggctctaatt	aattcctctg	180
gtttgttgaa	gcagttacca	agaatcttca	accctttccc	acaaaagcta	attgagtaca	240
cgttcctggt	gagtacacgt	tcctgttgat	ttacaaaagg	tcaggtatg	agcaggtctg	300
aagactaaca	ttttgtgaag	ttgtaaaaca	gaaaacctgt	tagaa atg tgg tgg ttt		357

Met Trp Trp Phe
 -20

cag	caa	ggc	ctc	agt	ttc	ctt	cct	tca	gcc	ctt	gta	att	tgg	aca	tct	405
Gln	Gln	Gly	Leu	Ser	Phe	Leu	Pro	Ser	Ala	Leu	Val	Ile	Trp	Thr	Ser	

-15 -10 -5

gct	gct	ttc	ata	ttt	tca	tac	att	act	gca	gta	aca	ctc	cac	cat	ata	453
Ala	Ala	Phe	Ile	Phe	Ser	Tyr	Ile	Thr	Ala	Val	Thr	Leu	His	His	Ile	

1 5 10 15

gac	ccg	gct	tta	cct	tat	atc	agt	gac	act	ggt	aca	gta	gct	cca	gaa	501
Asp	Pro	Ala	Leu	Pro	Tyr	Ile	Ser	Asp	Thr	Gly	Thr	Val	Ala	Pro	Glu	

20 25 30

aaa	tgc	tta	ttt	ggg	gca	atg	cta	aat	att	gcg	gca	ggt	tta	tgc	att	549
Lys	Cys	Leu	Phe	Gly	Ala	Met	Leu	Asn	Ile	Ala	Ala	Val	Leu	Cys	Ile	

35 40 45

gct	acc	att	tat	ggt	cgt	tat	aag	caa	ggt	cat	gct	ctg	agt	cct	gaa	597
Ala	Thr	Ile	Tyr	Val	Arg	Tyr	Lys	Gln	Val	His	Ala	Leu	Ser	Pro	Glu	

50 55 60

gag	aac	ggt	atc	atc	aaa	tta	aac	aag	gct	ggc	ctt	gta	ctt	gga	ata	645
Glu	Asn	Val	Ile	Ile	Lys	Leu	Asn	Lys	Ala	Gly	Leu	Val	Leu	Gly	Ile	

65 70 75

ctg	agt	tgt	tta	gga	ctt	tct	att	gtg	gca	aac	ttc	cag	gaa	aac	aac	693
Leu	Ser	Cys	Leu	Gly	Leu	Ser	Ile	Val	Ala	Asn	Phe	Gln	Glu	Asn	Asn	

80 85 90 95

cct	ttt	tgc	tgc	aca	tgt	aag	tgg	agc	tgt	gct	tac	ctt	tgg	tat	ggg	741
Pro	Phe	Cys	Cys	Thr	Cys	Lys	Trp	Ser	Cys	Ala	Tyr	Leu	Trp	Tyr	Gly	

100 105 110

```

ctc att ata tat gtt tgt tca gac cat cct ttc cta cca aaa tgc agc      789
Leu Ile Ile Tyr Val Cys Ser Asp His Pro Phe Leu Pro Lys Cys Ser
      115                      120                      125
cca aaa tcc aat ggc aaa aca agt ctt ctg gat cag act gtt gtt ggt      837
Pro Lys Ser Asn Gly Lys Thr Ser Leu Leu Asp Gln Thr Val Val Gly
      130                      135                      140
tat ctg gtg tgg agt aag tgc act tagcatgctg acttgctcat cagttttgca      891
Tyr Leu Val Trp Ser Lys Cys Thr
      145                      150
cagtggcaat tttgggactg atttagaaca gaaactccat tgggaaccccg aggacaaagg      951
ttatgcgctt cacatgatca ctactgcagc agaatgggtct atgtcatttt ccttcctttgg      1011
ttttttcctg acttacattc gtgattttca gaaaattttcc ttacgggtgg aagccaactt      1071
acatggatta accctctatg acaactgcacc ttgccctatt aacaatgaac gaacacggct      1131
actttccags aagatattag atgaaaggat aaaatatttc tgtaantgan ttastgastt      1191
ctcagggant tggggaaang gttcacagaa gttgcttavl tcttcacrtc gaanattttc      1251
aanccactta antcaaggct gacagstaac acgtgatgaa tgctgataat caggaaacat      1311
gaaagaagcc atttgcatag attattytaa aggatatcat caagaagamt attaaaaaca      1371
cctatgccta tactttttta tytcagaaaa taaagtcaaa agactatgaa aaaaaaaaaa      1431
aa                                                                1433

```

<210> 50

<211> 1158

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 214..339

<223> Von Heijne matrix

score 6.09999990463257

seq AILLLQSQAYWA/LP

<221> polyA_signal

<222> 1133..1138

<221> polyA_site

<222> 1146..1158

<221> misc_feature

<222> 840..968

<223> homology

id :H64717

est

<221> misc_feature

<222> 858..968

<223> homology

id :H65208

est

<400> 50

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aarttgagct tggggactgc agctgtgggg agatttcagt gcattgcctc ccctgggtgc      60
tcttcacrtt ggatttgaaa gttgagagca gcatgttttg cccactgaaa ctcatcctgs      120
tgrsagtgta mtggattatt ccttgggcct gaatgacttg aatgtttccc cgcctgagct      180
aacagtccat gtgggtgatt cagctctgat ggg atg tgt ttt cca gag cac aga      234
Met Cys Phe Pro Glu His Arg

```

-40

```

aga caa atg tat att caa gat aga ctg gac tct gtc acc agg aga gca      282
Arg Gln Met Tyr Ile Gln Asp Arg Leu Asp Ser Val Thr Arg Arg Ala
-35          -30          -25          -20
cgc caa gga cga ata tgt gct ata cta tta ctc caa tct cag tgt gcc      330
Arg Gln Gly Arg Ile Cys Ala Ile Leu Leu Leu Gln Ser Gln Cys Ala
          -15          -10          -5
tat tgg gcg ctt cca gaa ccg cgt aca ctt gat ggg gga cat ctt atg      378
Tyr Trp Ala Leu Pro Glu Pro Arg Thr Leu Asp Gly Gly His Leu Met
          1          5          10
caa tgatggctct ctctgtctcc aagatgtgca agaggctgac cagggaacct      431
Gln
atatctgtga aatccgcctc aaaggggaga gccagggtgtt caagaaggcg gtggtactgc      491
atgtgcttcc agaggagccc aaaggtacgc aaatgcttac ttaaagaggg gccaaggggc      551
aagagctttc atgtgcaaga ggcaaggaaa ctgattatct tgagtaaagt ccagcctttg      611
ggctaagtac ttaccacaga gtgaatcttc aaagaaatga ntcattaaat tatttcagrt      671
cagaataaaa atakgagtta ttttagttaa kaataaaaata ttgataatta ttgtattatt      731
actttaaaca cacttcccc tcacaaaagc cctgtgaagg atgttttggt cacatataat      791
gtccaaatat gttttggaca catattttatt aaatggaata aatagtamtt gaaccctggc      851
accthtgaca acaaaagtcya tgtyttttt actatgccct aataccttts atcagttatc      911
cacattgatg ctacatygtg attttatagg taccctatgt taggtgtttt gggggataga      971
aaagaaataa gcagkycagg ctcaagtggc catgcctgta atcctagcat tttgggaggc     1031
tgaggcagca gaamtgcctg agcccaggg ttcaagactg cagtgaagcta tgawggcacc     1091
actgcattyt agcctgggwg acagagcaag actygtttaa aaataaaaaa agagaaaaaa     1151
aaaaaaa

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<210> 51
<211> 850
<212> DNA
<213> Homo sapiens

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<220>
<221> sig_peptide
<222> 372..437
<223> Von Heijne matrix
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      seq LFLTCLFWPLAAL/NV

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<221> polyA_signal
<222> 812..817

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<221> polyA_site
<222> 838..850

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<221> misc_feature
<222> 128..424
<223> homology
      id :N78012
      est

```

```

<221> misc_feature
<222> 61..128
<223> homology
      id :N78012
      est

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<221> misc_feature
<222> 483..554

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<223> homology
id :N78012
est

<221> misc_feature
<222> 417..464
<223> homology
id :N78012
est

<221> misc_feature
<222> 460..500
<223> homology
id :N78012
est

<221> misc_feature
<222> 577..612
<223> homology
id :N78012
est

<221> misc_feature
<222> 612..649
<223> homology
id :N78012
est

<221> misc_feature
<222> 546..577
<223> homology
id :N78012
est

<221> misc_feature
<222> 29..63
<223> homology
id :N78012
est

<221> misc_feature
<222> 128..294
<223> homology
id :W37233
est

<221> misc_feature
<222> 370..509
<223> homology
id :W37233
est

<221> misc_feature
<222> 505..591
<223> homology
id :W37233
est

<221> misc_feature
 <222> 293..330
 <223> homology
 id :W37233
 est

<221> misc_feature
 <222> 22..57
 <223> homology
 id :W37233
 est

<221> misc_feature
 <222> 95..128
 <223> homology
 id :W37233
 est

<221> misc_feature
 <222> 128..326
 <223> homology
 id :AA186399
 est

<221> misc_feature
 <222> 418..605
 <223> homology
 id :AA186399
 est

<221> misc_feature
 <222> 326..423
 <223> homology
 id :AA186399
 est

<221> misc_feature
 <222> 39..128
 <223> homology
 id :AA186399
 est

<221> misc_feature
 <222> 206..640
 <223> homology
 id :W52489
 est

<400> 51
 agacacttcc tgggtgggac cgagtgaggc gacggggtag gggttggcgc tcaggcggcg 60
 accatggcgt atcacggcct cactgtgcct ctcatgtga tgagcgtgtt ctggggcttc 120
 gtgcgctttc ttggtgcctt ggttcacccc taaggggcct aaccggggag ttatcattac 180
 catgttggtg acctgttcag tttgctgcta tctcttttgg ctgattgcaa ttctggccca 240
 actcaaccct ctctttggac cgcaattgaa aaatgaaacc atctggatc tgaagtatca 300
 ttggccttga ggaagaagac atgctctaca gtgctcagtc tttgagggtca cgagaagaga 360
 atgccttcta g atg caa aat cac ctc caa acc aga cca ctt ttc ttg act 410
 Met Gln Asn His Leu Gln Thr Arg Pro Leu Phe Leu Thr
 -20 -15 -10

tgc ctg ttt tgg cca tta gct gcc tta aac gtt aac agc aca ttt gaa	458
Cys Leu Phe Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu	
-5 1 5	
tgc ctt att cta caa tgc agc gtg ttt tcc ttt gcc ttt ttt gca ctt	506
Cys Leu Ile Leu Gln Cys Ser Val Phe Ser Phe Ala Phe Phe Ala Leu	
10 15 20	
tgg tgaattacgt gctccataa cctgaactgt gccgactcca caaaacgatt	559
Trp	
atgtactctt ctgagataga agatgctggt cttctgagag atacgttact ctctccttgg	619
aatctgtgga tttgaaaatg gctcctgcct tctcacgtgg gaatcagtga agtggttaga	679
aactgctgca agacaaacaa gactccagtg ggggtggtcag taggaaaaca cgttcagagg	739
gaagaacccat ctcaacagaa tcgcaccaa ctatactttc aggatgaatt tcttctttct	799
gccatctttt ggaataaata ttttctctct ttttatgtaa aaaaaaaaaa a	850

<210> 52
 <211> 1107
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 132..215
 <223> Von Heijne matrix
 score 3.59999990463257
 seq PLSDSWALLPASA/GV

<221> polyA_signal
 <222> 1069..1074

<221> polyA_site
 <222> 1094..1107

<221> misc_feature
 <222> 177..392
 <223> homology
 id :W80978
 est

<221> misc_feature
 <222> 425..542
 <223> homology
 id :W80978
 est

<221> misc_feature
 <222> 43..114
 <223> homology
 id :W80978
 est

<221> misc_feature
 <222> 387..441
 <223> homology
 id :W80978
 est

<221> misc_feature

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<222> 113..165
<223> homology
      id :W80978
      est

<221> misc_feature
<222> 551..590
<223> homology
      id :W80978
      est

<221> misc_feature
<222> 166..314
<223> homology
      id :AA043154
      est

<221> misc_feature
<222> 27..181
<223> homology
      id :AA043154
      est

<221> misc_feature
<222> 425..564
<223> homology
      id :AA043154
      est

<221> misc_feature
<222> 387..441
<223> homology
      id :AA043154
      est

<221> misc_feature
<222> 309..352
<223> homology
      id :AA043154
      est

<221> misc_feature
<222> 549..580
<223> homology
      id :AA043154
      est

<221> misc_feature
<222> 601..1071
<223> homology
      id :AA126732
      est

<221> misc_feature
<222> 576..605
<223> homology
      id :AA126732
      est

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<221> misc_feature
 <222> 387..477
 <223> homology
 id :AA161280
 est

<221> misc_feature
 <222> 292..362
 <223> homology
 id :AA161280
 est

<221> misc_feature
 <222> 46..113
 <223> homology
 id :AA161280
 est

<221> misc_feature
 <222> 217..277
 <223> homology
 id :AA161280
 est

<221> misc_feature
 <222> 113..160
 <223> homology
 id :AA161280
 est

<221> misc_feature
 <222> 173..217
 <223> homology
 id :AA161280
 est

<400> 52

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aacaacttcc ggccccactg agcgggtgtcc tgagccgatt acagctaggt agtggagcgc      60
cgctgcttac ctgggtgcag gagacagccg gagtcgctgg gggagctccg cgccgccgga      120
cgcccggtgac c atg tgg agg ctg ctg gct cgc gct agt gcg ccg ctc ctg      170
               Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu
               -25                               -20

cgg gtg ccc ttg tca gat tcc tgg gca ctc ctc ccc gcc agt gct ggc      218
Arg Val Pro Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly
-15                               -10                               -5                               1
gta aag aca ctg ctc cca gta cca agt ttt gaa gat gtt tcc att cct      266
Val Lys Thr Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro
               5                               10                               15

gaa aaa ccc aag ctt aga ttt att gaa agg gca cca ctt gtg cca aaa      314
Glu Lys Pro Lys Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys
               20                               25                               30

gta aga aga gaa cct aaa aat tta agt gac ata cgg gga cct tcc act      362
Val Arg Arg Glu Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr
               35                               40                               45

gaa gct acg gag kkk aca gaa ggc aat ttt gca atc ttg gca ttg ggt      410
Glu Ala Thr Glu Xaa Thr Glu Gly Asn Phe Ala Ile Leu Ala Leu Gly
50                               55                               60                               65

```

```

ggt ggc tac ctg cat tgg ggc cac ttt gaa atg atg cgc ctg aca atc      458
Gly Gly Tyr Leu His Trp Gly His Phe Glu Met Met Arg Leu Thr Ile
      70      75      80
aac cgc tct atg gac ccc aag aac atg ttt gcc ata tgg cga gta cca      506
Asn Arg Ser Met Asp Pro Lys Asn Met Phe Ala Ile Trp Arg Val Pro
      85      90      95
gcc cct ttc aag ccc atc act cgc aaa agt gtt ggg cat cgc atg ggg      554
Ala Pro Phe Lys Pro Ile Thr Arg Lys Ser Val Gly His Arg Met Gly
      100      105      110
gga ggc aaa ggt gct att gac cac tac gtg aca cct gtg aag gct ggc      602
Gly Gly Lys Gly Ala Ile Asp His Tyr Val Thr Pro Val Lys Ala Gly
      115      120      125
cgc mww gww gta gag atg ggt ggg cgt tgt gma ttt gaa gaa gtg caa      650
Arg Xaa Xaa Val Glu Met Gly Gly Arg Cys Xaa Phe Glu Glu Val Gln
      130      135      140      145
ggt ttc ctt gac cag gtt gcc cac aag ttg ccc tty gca gca aag gct      698
Gly Phe Leu Asp Gln Val Ala His Lys Leu Pro Phe Ala Ala Lys Ala
      150      155      160
gtg agc cgc ggg act yta gag aag atg cga aaa gat caa gag gaa aga      746
Val Ser Arg Gly Thr Leu Glu Lys Met Arg Lys Asp Gln Glu Glu Arg
      165      170      175
gaa mgt aac aac cag aac ccc tgg aca ttt gag cga ata gcc act gcc      794
Glu Xaa Asn Asn Gln Asn Pro Trp Thr Phe Glu Arg Ile Ala Thr Ala
      180      185      190
mac atg ctg ggc ata cgg aaa gta ctg agc cca tat gac ttg acc cac      842
Xaa Met Leu Gly Ile Arg Lys Val Leu Ser Pro Tyr Asp Leu Thr His
      195      200      205
aag ggg aaa tam tgg ggc aag tty tac atg ccc mam cgt gtg      884
Lys Gly Lys Xaa Trp Gly Lys Phe Tyr Met Pro Xaa Arg Val
      210      215      220
tagtgagtgt aggagataac tgtatatagg stactgaaag aaggattytg catttytatt      944
cccctcagcc taccactga agtytttggg tagctytaa gccataamta aggagcagca      1004
tttgagtaga ttttgaaaa acgatgttat ttgttgattt aaaaagaaaa cwgtattttt      1064
attaaataaa atttaaacad cacttcagga aaaaaaaaaaaa aaa      1107

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<210> 53

<211> 500

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 199..288

<223> Von Heijne matrix

score 5.59999990463257

seq IVSVLALIPETTT/LT

<221> polyA_signal

<222> 464..469

<221> polyA_site

<222> 489..500

<221> misc_feature

<222> 197..412

<223> homology

id :AA429945

est

<221> misc_feature
<222> 61..195
<223> homology
id :AA429945
est

<221> misc_feature
<222> 425..488
<223> homology
id :AA429945
est

<221> misc_feature
<222> 197..412
<223> homology
id :AA455042
est

<221> misc_feature
<222> 61..195
<223> homology
id :AA455042
est

<221> misc_feature
<222> 425..488
<223> homology
id :AA455042
est

<221> misc_feature
<222> 207..412
<223> homology
id :W93646
est

<221> misc_feature
<222> 58..195
<223> homology
id :W93646
est

<221> misc_feature
<222> 425..488
<223> homology
id :W93646
est

<221> misc_feature
<222> 197..412
<223> homology
id :AA516431
est

<221> misc_feature
<222> 90..195

<223> homology
id :AA516431
est

<221> misc_feature
<222> 425..488
<223> homology
id :AA516431
est

<221> misc_feature
<222> 52..195
<223> homology
id :W38899
est

<221> misc_feature
<222> 197..324
<223> homology
id :W38899
est

<221> misc_feature
<222> 443..477
<223> homology
id :W38899
est

<221> misc_feature
<222> 197..338
<223> homology
id :W52820
est

<221> misc_feature
<222> 71..195
<223> homology
id :W52820
est

<221> misc_feature
<222> 339..401
<223> homology
id :W52820
est

<221> misc_feature
<222> 425..469
<223> homology
id :W52820
est

<221> misc_feature
<222> 40..195
<223> homology
id :W19506
est

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<400> 53
agagctgtnn cnsaagtagg ggagggcggt gctccgcmgm ggtggcggdh tgctatcgct      60
tcgcagaacc tactcaggca gccagctgag aagagttgag ggaaagtgct gctgctgggt      120
ctgcagacgc gatggataac gtgcagccga aaataaaaaca tcgccccttc tgcttcagtg      180
tgaaaggcca cgtgayag atg ctg cggtg gat att atc aac tca ctg gta      231
                Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val
                -30                -25                -20
aca aca gta ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa      279
Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu
                -15                -10                -5
acc aca aca ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca      327
Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala
                1                5                10
gta tgc tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc      375
Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe
                15                20                25
aat ccc agc ggt cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa      423
Asn Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
                30                35                40                45
gtt ttg taattttata ttacttttta gtttgatact aagtattaaa catatttctg      479
Val Leu
tattcttcca aaaaaaaaaa a      500

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<210> 54
<211> 765
<212> DNA
<213> Homo sapiens

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<220>
<221> sig_peptide
<222> 293..385
<223> Von Heijne matrix
      score 4.40000009536743
      seq TCCHLGLPHPVRA/PR

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<221> polyA_signal
<222> 733..738
<221> polyA_site
<222> 752..765

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<221> misc_feature
<222> 310..576
<223> homology
      id :HUM426A07B
      est

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<400> 54
aaaccttggt gctagggacc gggcggtttg cggcaaccgt gggcactgct gaatttgaat      60
tgaggggcca gggaaaagt ttccctcagg gtggtgggga gagggaggcg gatgccgng      120
aaaccgtagg kacgcggtca gaaaggcgac gggctgtcgg agttggaaag ggacgcctgg      180
tttcccccca agcgaaccgg gatgggaagt gacttcaatg agattgaact tcagctggat      240
tgaaagagag gctagaagtt ccgcttgcca gcagcctcct tagtagagcg ga atg agt      298
                Met Ser
                -30
aat acc cac acg gtg ctt gtc tca ctt ccc cat ccg cac ccg gcc ctc      346
Asn Thr His Thr Val Leu Val Ser Leu Pro His Pro His Pro Ala Leu

```


	-25		-20		-15	
acc tgc tgt cac ctc ggc ctc cca cac ccg gtc cgc gct ccc cgc cct						394
Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro Arg Pro						
	-10		-5		1	
ctt cct cgc gta gaa ccg tgg gat cct agg tgg cag gac tca gag cta						442
Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser Glu Leu						
	5		10		15	
agg tat cca cag gcc atg aat tcc ttc cta aat gag cgg tca tcg ccg						490
Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser Ser Pro						
	20		25		30	35
tgc agg acc tta agg caa gaa gca tcg gct gac aga tgt gat ctc						535
Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp Leu						
	40		45		50	
tgaacctgat agattgctga ttttatctta ttttatcctt gacttggtac aagttttggg						595
attttctgaaa agaccataca gataaccaca aatatcaaga aagtcgtctt cagtattaag						655
tagaatttag atttaggttt ctttctgct tcccacctcc ttcgaataag gaaacgtctt						715
tgggaccaac tttatggaat aaataagctg agctgcaaaa waaaaaaaaa						765

<210> 55

<211> 584

<212> DNA

<213> Homo sapiens

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<221> sig_peptide

<222> 130..189

<223> Von Heijne matrix

score 3.5

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<222> 546..551

<221> polyA_site

<222> 572..584

<400> 55

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gtgcagccgg ggtttggtac cgagcggaga ggagatgcac acggcactcg agtgtgagga	120
aaaatagaa atg aag gta cat atg cac aca aaa ttt tgc ctc att tgt ttg	171
Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu	
	-20 -15 -10
ctg aca ttt att ttt cat cat tgc aac cat tgc cat gaa gaa cat gac	219
Leu Thr Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp	
	-5 1 5 10
cat ggc cct gaa gcg ctt cac aga cag cat cgt gga atg aca gaa ttg	267
His Gly Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu Leu	
	15 20 25
gag cca agc aaa ttt tca aag caa gct gct gaa aat gaa aaa aaa tac	315
Glu Pro Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys Tyr	
	30 35 40
tat att gaa aaa ctt ttt gag cgt tat ggt gaa aat gga aga tta tcc	363
Tyr Ile Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu Ser	
	45 50 55
ttt ttt ggt ttg gag aaa ctt tta aca aac ttg ggc ctt gga gag aga	411
Phe Phe Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu Arg	
	60 65 70

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<211> 1387
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<222> 1348..1353
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<223> homology
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      est
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<222> 1258..1372
<223> homology
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      est
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<223> homology
id :AA480326
est

<221> misc_feature
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
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est

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<221> misc_feature
<222> 94..268
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ttccccgaaa	accttccccg	cttctggata	tgaavattca	agctgcttgc	tgagtcctat	120
tgccgggtgc	tgggagccag	gagagccctg	aggagtagtc	actcagtagc	agctgacgcg	180
tgggtccacc	atg aac tgg agt atc ttt gag gga ctc ctg agt ggg gtc	229				
	Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val					
	-45 -40 -35					
aac aag tac tcc aca gcc ttt ggg cgc atc tgg ctg tct ctg gtc ttc	277					
Asn Lys Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe						
-30 -25 -20						
atc ttc cgc gtg ctg gtg tac ctg gtg acg gcc gag cgt gtg tgg agt	325					
Ile Phe Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser						
-15 -10 -5						
gat gac cac aag gac ttc gac tgc aat act cgc cag ccc ggc tgc tcc	373					
Asp Asp His Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser						
1 5 10 15						
aac gtc tgc ttt gat gag ttc ttc cct gtg tcc cat gtg cgc ctc tgg	421					
Asn Val Cys Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp						
20 25 30						
gcc ctg cag ctt atc ctg gtg aca tgc ccc tca ctg ctc gtg gtc atg	469					
Ala Leu Gln Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met						
35 40 45						
cac gtg gcc tac cgg gag gtt cag gag aag agg cac cga gaa gcc cat	517					
His Val Ala Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His						
50 55 60						
ggg gag aac agt ggg cgc ctc tac ctg aac ccc ggc aag aar cgg ggt	565					
Gly Glu Asn Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly						
65 70 75 80						
ggg ctc tgg tgg aca tat gtc tgc agc cta gtg ttc aag gcg agc gtg	613					
Gly Leu Trp Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val						
85 90 95						
gac atc gcc ttt ctc tat gtg ttc cac tca ttc tac ccc aaa tat atc	661					
Asp Ile Ala Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile						
100 105 110						
ctc cct cct gtg gtc aag tgc cac gca gat cca tgt ccc aat ata gtg	709					
Leu Pro Pro Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val						
115 120 125						
gac tgc ttc atc tcc aag ccc tca gag aag aac att ttc acc ctc ttc	757					

Asp Cys Phe Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe	
130 135 140	
atg gtg gcc aca gct gcc atc tgc atc ctg ctc aac ctc gtg gag ctc	805
Met Val Ala Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu	
145 150 155 160	
atc tac ctg gtg agc aag aga tgc cac gag tgc ctg gca gca agg aaa	853
Ile Tyr Leu Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys	
165 170 175	
gct caa gcc atg kgc aca ggt cat cac ccc cav gat acc acy ttt tcc	901
Ala Gln Ala Met Xaa Thr Gly His His Pro Xaa Asp Thr Thr Phe Ser	
180 185 190	
kgc aaa caa gas gac ytc ytt tcg ggk gac ytc atc ttt ctg ggn tca	949
Xaa Lys Gln Xaa Asp Xaa Xaa Ser Gly Asp Xaa Ile Phe Leu Gly Ser	
195 200 205	
gac agt cat cyt cct ytc tta cca gac cgc ccc cga gac cat gtg aag	997
Asp Ser His Xaa Pro Xaa Leu Pro Asp Arg Pro Arg Asp His Val Lys	
210 215 220	
aaa acc aty ttg tgaggggctg cctggamtgg tytggcaggt tgggcctgga	1049
Lys Thr Ile Leu	
225	
tggggagggt ytagcatyty tcataggtgc aacctgagag tgggggagct aagccatgag	1109
gtagggggcag gcaagagaga ggattcagac gytytgggag ccagttccta gtcctcaamt	1169
ccagccacct gccccagsth gacggcamtg ggccagttcc ccctytgsty tgcagstcgg	1229
tttcctttty tagaatggaa atagtgaggg ccaatgccca gggttggagg gaggagggcg	1289
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<222> 141..251

<223> Von Heijne matrix

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<222> 1354..1359

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<222> 1375..1385

<221> misc_feature

<222> 1183..1240

<223> homology

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est

<221> misc_feature

<222> 176..239

<223> homology

id :AA258927

est

<221> misc_feature
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 <223> homology
 id :AA286417
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<221> misc_feature
 <222> 1183..1213
 <223> homology
 id :AA608077
 est

<400> 57

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aagccatcca ggggtcttta accagaagag agaggagagc ctcaggagtt aggaccagaa      120
gaagccaggg aagcagtgca atg gct tca aaa atc ttg ctt aac gta caa gag      173
                               Met Ala Ser Lys Ile Leu Leu Asn Val Gln Glu
                               -35                               -30

gag gtg acc tgt ccc atc tgc ctg gag ctg ttg aca gaa ccc ttg agt      221
Glu Val Thr Cys Pro Ile Cys Leu Glu Leu Leu Thr Glu Pro Leu Ser
-25                               -20                               -15

cta gac tgt ggc cac agc ctc tgc cga gcc tgc atc act gtg agc aac      269
Leu Asp Cys Gly His Ser Leu Cys Arg Ala Cys Ile Thr Val Ser Asn
-10                               -5                               1                               5

aaag gag gca gtg acc agc atg gga gga aaa agc agc tgt cct gtg tgt      317
Lys Glu Ala Val Thr Ser Met Gly Gly Lys Ser Ser Cys Pro Val Cys
                               10                               15                               20

gggt atc agt tac tca ttt gaa cat cta cag gct aat cag cat cgg gcc      365
Gly Ile Ser Tyr Ser Phe Glu His Leu Gln Ala Asn Gln His Arg Ala
25                               30                               35

aac ata gtg gag aga ctc aag gag gtc aag ttg agc cca gac aat ggg      413
Asn Ile Val Glu Arg Leu Lys Glu Val Lys Leu Ser Pro Asp Asn Gly
40                               45                               50

aag aag aga gat ctc tgt gat cat cat gga gag aaa ctc cta ctc ttc      461
Lys Lys Arg Asp Leu Cys Asp His His Gly Glu Lys Leu Leu Leu Phe
55                               60                               65                               70

tgt aag gag gat agg aaa gtc att tgc tgg ctt tgt gag cgg tct cag      509
Cys Lys Glu Asp Arg Lys Val Ile Cys Trp Leu Cys Glu Arg Ser Gln
75                               80                               85

gag cac cgt ggt cac cac aca ggt cct cac gga gga agt att caa gga      557
Glu His Arg Gly His His Thr Gly Pro His Gly Gly Ser Ile Gln Gly
90                               95                               100

atg tca gga gaa act cca ggc agt cct caa gag gct gaa gaa gga aga      605
Met Ser Gly Glu Thr Pro Gly Ser Pro Gln Glu Ala Glu Glu Gly Arg
105                               110                               115

gga gga agc tgagaagctg gaagctgaca tcagagaaga gaaaacttcc      654
Gly Gly Ser
120

tggaagtatc aggtacaaac tgagagacaa aggatacaaa cagaatttga tcagcttaga      714
agcatcctaa ataatgagga gcagagagag ctgcaaagat tggaagaaga agaaaagaag      774
acgctggata agtttgcaga ggctgaggat gagctagttc agcagaagca gttggtgaga      834
gagctcatct cagatgtgga gtgtcggagt cagtgggtcaa caatggagct gctgcaggac      894
atgagtggaa tcatgaaatg gagtggatgc tggaggctga aaaagccaaa aatggtttcc      954
aagaaactga agactgtatt ccatgctcca gatctgagta ggatgctgcr aatgtttaga      1014
ggaactgaca gctgtccggg gctactgggt ggatgtcaca ctgaattcag tcaacctaaa      1074
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tggaagtgg acgtgtccaa gaaaactgcc tggatcctgg gggatatactg tagaacatat      1254

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tcccgccata tgaagtatgt tgtagaaga tgtgcaaaty gtcaaatbt ttacaccaa	1314
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aaaaaaaaa a	1385

<210> 58
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 <222> 212..268
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<221> misc_feature
 <222> 958..1110
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agactgggtg cctgggagct gaggcagcca ccgtttcagc ctggccagcc ctctggaccc 180
cgaggttgga ccctactgtg acacacctac c atg cgg aca ctc ttc aac ctc 232
Met Arg Thr Leu Phe Asn Leu
-15
ctc tgg ctt gcc ctg gcc tgc agc cct gtt cac act acc ctg tca aag 280
Leu Trp Leu Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys
-10 -5 1
tca gat gcc asa aaa ccg cct caa aga cgc tgc tgg aga aga gtc agt 328
Ser Asp Ala Xaa Lys Pro Pro Gln Arg Arg Cys Trp Arg Arg Val Ser
5 10 15 20
ttt cag ata agc cgg tgc aar acc ggg gtt tgg tgg tgacggacct 374
Phe Gln Ile Ser Arg Cys Lys Thr Gly Val Trp Trp
25 30
caaagctgag agtgtggttc ttgagcatcg cagctactgc tcggcaaagg cccgggacag 434
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acgtggccgt gagatgtttg aggtcacggg cctccacgac gtggaccaag ggtggatgcg 614
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ctgtttgtcgg ggccagggtac atccagacac tgaadggacc acaggccccg ggaatggtgt 1214
gggacagcca ggccctcagag cacttcttcg agtacaagaa gagccgcagt gggaggcacg 1274

tcgtcttcta	cccaaccctg	aagtcctgc	aggtgcgggc	tggagctggc	ccgggagctg	1334
ggcgttgggg	tctctatytg	ggagctgggc	cagggcctgg	actacttyta	cgacctgcty	1394
taggtgggca	ttgcggcctc	cgcggtggac	gtgttytttt	ytaagccatg	gagtgagtga	1454
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<221> misc_feature
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<223> homology
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<221> misc_feature
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 gaacttcaag gtgattttac aacgag atg ctg ctc tcc ata ggg atg ctc atg 173
 Met Leu Leu Ser Ile Gly Met Leu Met
 -30
 ctg tca gcc aca caa gtc tac acc atc ttg act gtc cag ctc ttt gca 221
 Leu Ser Ala Thr Gln Val Tyr Thr Ile Leu Thr Val Gln Leu Phe Ala
 -25 -20 -15 -10
 ttc tta aac cta ctg cct gta gaa gca gac att tta gca tat aac ttt 269
 Phe Leu Asn Leu Leu Pro Val Glu Ala Asp Ile Leu Ala Tyr Asn Phe
 -5 1 5
 gaa aat gca tct cag aca ttt gat gac ctc ccc gca ara ttt ggt tat 317
 Glu Asn Ala Ser Gln Thr Phe Asp Asp Leu Pro Ala Xaa Phe Gly Tyr
 10 15 20
 aga ctt cca gct gaa ggt tta aag ggt ttt tta att aac tca aaa cca 365
 Arg Leu Pro Ala Glu Gly Leu Lys Gly Phe Leu Ile Asn Ser Lys Pro
 25 30 35
 gag aat gcc tgt gaa ccc ata gtg cct cca cca gta aaa gac aat tca 413
 Glu Asn Ala Cys Glu Pro Ile Val Pro Pro Pro Val Lys Asp Asn Ser
 40 45 50 55
 tct ggc act ttc atc gtg tta att ara ara ctt gat tgt aat ttt gat 461
 Ser Gly Thr Phe Ile Val Leu Ile Xaa Xaa Leu Asp Cys Asn Phe Asp
 60 65 70
 ata aag gtt tta aat gca cag aga gca gga tac aag gca gcc ata gtt 509
 Ile Lys Val Leu Asn Ala Gln Arg Ala Gly Tyr Lys Ala Ala Ile Val
 75 80 85
 cac aat gtt gat tct gat gac ctc att agc atg gga tcc aac gac att 557
 His Asn Val Asp Ser Asp Asp Leu Ile Ser Met Gly Ser Asn Asp Ile
 90 95 100

gag gta cta aag aaa att gac att cca tct gtc ttt att ggt gaa tca	605
Glu Val Leu Lys Lys Ile Asp Ile Pro Ser Val Phe Ile Gly Glu Ser	
105 110 115	
tca gct agt tct ctg aaa gat gaa ttc aca tak gaa aaa ggg ggc cac	653
Ser Ala Ser Ser Leu Lys Asp Glu Phe Thr Xaa Glu Lys Gly Gly His	
120 125 130 135	
ctt atc tta gtt cca gaa ttt agt ctt cct ttg gaa tac tac cta att	701
Leu Ile Leu Val Pro Glu Phe Ser Leu Pro Leu Glu Tyr Tyr Leu Ile	
140 145 150	
ccc ttc ctt atc atr gtg ggc atc tgt ctc atc ttg ata gtc att ttc	749
Pro Phe Leu Ile Xaa Val Gly Ile Cys Leu Ile Leu Ile Val Ile Phe	
155 160 165	
atg atc aca aaa ttg tcc agg gat aga cat aga gct aga aac aga	797
Met Ile Thr Lys Leu Ser Arg Asp Arg His Arg Ala Arg Arg Asn Arg	
170 175 180	
ctt cgt aaa gat caa ctt aag aaa ctt cct gta cat aaa ttc aag aaa	845
Leu Arg Lys Asp Gln Leu Lys Lys Leu Pro Val His Lys Phe Lys Lys	
185 190 195	
gga gat gag tat gat gta tgt gcc att tgt ttg gat gag tat gaa gat	893
Gly Asp Glu Tyr Asp Val Cys Ala Ile Cys Leu Asp Glu Tyr Glu Asp	
200 205 210 215	
gga gac aaa ctc aga atc ctt ccc tgt tcc cat gct tat cat tgc aag	941
Gly Asp Lys Leu Arg Ile Leu Pro Cys Ser His Ala Tyr His Cys Lys	
220 225 230	
tgt gta gac cct tgg cta act aaa acc aaa acc tgt cca gtg tgc	989
Cys Val Asp Pro Trp Leu Thr Lys Thr Lys Lys Thr Cys Pro Val Cys	
235 240 245	
agg caa aaa gtt gtt cct tct caa ggc gat tca gac tct gac aca gac	1037
Arg Gln Lys Val Val Pro Ser Gln Gly Asp Ser Asp Ser Asp Thr Asp	
250 255 260	
agt agt caa gaa gaa aat gaa gtg aca gaa cat acc cct tta ctg aga	1085
Ser Ser Gln Glu Glu Asn Glu Val Thr Glu His Thr Pro Leu Leu Arg	
265 270 275	
cct tta gnc ttc tgt cag tgc cca rgt cam ttt ggg gct tta ntc gga	1133
Pro Leu Xaa Phe Cys Gln Cys Pro Xaa Xaa Phe Gly Ala Leu Xaa Gly	
280 285 290 295	
ant ccc gct cac ant cag aak cat gac aga atc att cag act ast gag	1181
Xaa Pro Ala His Xaa Gln Xaa His Asp Arg Ile Ile Gln Thr Xaa Glu	
300 305 310	
gaa gac gac aat gaa gat act gac agt agt gat gca gaa gaa	1223
Glu Asp Asp Asn Glu Asp Thr Asp Ser Ser Asp Ala Glu Glu	
315 320 325	
tgaaattaat gaacatgatg tcgtggtcca gttgcagcct aatggtgaac gggattacaa	1283
catagcaaact actgttttgac tttcagaaga tgatttggttt atttcccttt aaaatgatta	1343
ggtatatact gtaatttgat tttttgctcc cttaaaagat ttytgtagaa ataacttatt	1403
ttttagtact ytacagttta atcaaattac tgaaacagga cttttgatyt ggtattttatc	1463
tgccaagaat atacttcatt cactaataat agactggtgc tgtaactcaa gcatcaattc	1523
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<221> polyA_site
 <222> 1010..1022

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                                     Met Asp

tct agg gtg tct tca cct gag aag caa gat aaa gag aat ttc gtg ggt      165
Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe Val Gly
-40                               -35                               -30                               -25

gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg atc ctg ttt tcc ctc      213
Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe Ser Leu
                               -20                               -15                               -10

tct ttc ctg ttg gtg atc att acc ttc ccc atc tcc ata tgg atg tgc      261
Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp Met Cys
                               -5                               1                               5

ttg aag atc att aag gag tat gaa cgt gct gtt gta ttc cgt ctg gga      309
Leu Lys Ile Ile Lys Glu Tyr Glu Arg Ala Val Phe Arg Leu Gly
10                               15                               20

cgc atc caa gct gac aaa gcc aag ggg cca ggt ttg atc ctg gtc ctg      357
Arg Ile Gln Ala Asp Lys Ala Lys Gly Pro Gly Leu Ile Leu Val Leu
25                               30                               35                               40

cca tgc ata gat gtg ttt gtc aag gtt gac ctc cga aca gtt act tgc      405
Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu Arg Thr Val Thr Cys
                               45                               50                               55

aac att cct cca caa gag atc ctc acc aga gac tcc gta act act cag      453
Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp Ser Val Thr Thr Gln
60                               65                               70

gta gat gga gtt gtc tat tac aga atc tat agt gct gtc tca gca gtg      501
Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser Ala Val Ser Ala Val
75                               80                               85

gct aat gtc aac gat gtc cat caa gca aca ttt ctg ctg gct caa acc      549
Ala Asn Val Asn Asp Val His Gln Ala Thr Phe Leu Leu Ala Gln Thr
90                               95                               100

act ctg aga aat gtc tta ggg aca cag acc ttg tcc cag atc tta gct      597
Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu Ser Gln Ile Leu Ala
105                               110                               115                               120

gga cga gaa gag atc gcc cat agc atc cag act tta ctt gat gat gcc      645
Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr Leu Leu Asp Asp Ala
125                               130                               135

acc gaa ctg tgg ggg atc cgg gtg gcc cga gtg gaa atc aaa gat gtt      693
Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val Glu Ile Lys Asp Val
140                               145                               150

cgg att ccc gtg cag ttg cag aga tcc atg gca gcc gag gct gag gcc      741
Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala Glu Ala
155                               160                               165

acc cgg gaa gcg aga gcc aag gtc ctt gca gct gaa gga gaa atg agt      789
Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu Met Ser
170                               175                               180

gct tcc aaa tcc ctg aag tca gcc tcc atg gtg ctg gct gag tct ccc      837
Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu Ser Pro

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185	190	195	200	
ata gct ctc cag ctg cgc tac ctg cag acc ttg agc acg gta gcc acc				885
Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val Ala Thr				
	205	210	215	
gag aag aat tct acg att gtg ttt cct ctg ccc atg aat ata cta gag				933
Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile Leu Glu				
	220	225	230	
ggc att ggt ggc gtc agc tat gat aac cac aag aag ctt cca aat aaa				981
Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro Asn Lys				
	235	240	245	
gcc tgaggctctc ttgcggtagt cagctaaaaa aaaaaaaa				1022
Ala				

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<221> misc_feature
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ctggataagt gctatgtgat ccctctgaac acttccattg ttatgccacc cagaaaccta      180
ctggagttac ttattaacat caaggctgga acctatttgc ctcagtccta tctgattc      238
atg agc aca tgg tta tta ctg atc gca ttg aaa aca ttg atc acc tgg      286
Met Ser Thr Trp Leu Leu Leu Ile Ala Leu Lys Thr Leu Ile Thr Trp
      -25                      -20                      -15
gtt tct tta ttt atc gac tgt gtc atg aca agg aaa ctt aca aac tgc      334
Val Ser Leu Phe Ile Asp Cys Val Met Thr Arg Lys Leu Thr Asn Cys
      -10                      -5                      1                      5
aac gct aga gaa act att aaa ggt att cag aaa cgt gaa gcc agc aat      382
Asn Ala Arg Glu Thr Ile Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn
      10                      15                      20
tgt ttc gca att cgg cat ttt gaa aac aaa ttt gcc gtg gaa act tta      430
Cys Phe Ala Ile Arg His Phe Glu Asn Lys Phe Ala Val Glu Thr Leu
      25                      30                      35
att tgt tct tgaacagtca agaaaaacat tattgaggaa aattaatatc      479
Ile Cys Ser
      40
acagcataac cccacccttt acattttgtg cagtgattat tttttaaagt cttctttcat      539
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<221> misc_feature
 <222> 425..790
 <223> homology
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 <222> 186..430
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<221> misc_feature
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<400> 62

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gctcccaccc ggctgcchaa ggatccctcg gcggcg atg tcg gcc gcc ggt gcc	174
Met Ser Ala Ala Gly Ala	
-60	
cga ggc ctg cgg gcc acc tac cac cgg ctc ctc gat aaa gtg gag ctg	222
Arg Gly Leu Arg Ala Thr Tyr His Arg Leu Leu Asp Lys Val Glu Leu	
-55 -50 -45	
atg ctg ccc gag aaa ttg agg ccg ttg tac aac cat cca gca ggt ccc	270
Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro	
-40 -35 -30	
aga aca gtt ttc ttc tgg gct cca att atg aaa tgg ggg ttg gtg tgt	318
Arg Thr Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys	
-25 -20 -15 -10	
gct gga ttg gct gat atg gcc aga cct gca gaa aaa ctt agc aca gct	366
Ala Gly Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala	
-5 1 5	
caa tct gct gtt ttg atg gct aca ggg ttt att tgg tca aga tac tca	414
Gln Ser Ala Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser	
10 15 20	
ctt gta att att ccg aaa aat tgg agt ctg ttt gct gtt aat ttc ttt	462
Leu Val Ile Ile Pro Lys Asn Trp Ser Leu Phe Ala Val Asn Phe Phe	
25 30 35	
gtg ggg gca gca gga gcc tct cag ctt ttt cgt att tgg aga tat aac	510
Val Gly Ala Ala Gly Ala Ser Gln Leu Phe Arg Ile Trp Arg Tyr Asn	
40 45 50 55	
caa gaa cta aaa gct aaa gca cac aaa taaaagagtt cctgatcacc	557
Gln Glu Leu Lys Ala Lys Ala His Lys	
60	
tgaacaatct agatgtggac aaaaccattg ggacctagtt tattatttgg ttattgataa	617
agcaaagcta actgtgtgtt tagaaggcac tgtaactggg agctagttct tgattcaata	677
gaaaaatgca gcaaactttt aataacagtc tctctacatg acttaaggaa cttatctatg	737

gatattagta acatttttct accatttgct cgtaataaaa catacttgct cgtaaaaaaa 797
aaaaaaa 804

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<222> 780..792

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cagcggctctt	ccagcgttg	ggccacggcg	gcggccctgg	gagcagaggt	ggagcgaccc	180
cattacgcta	aag atg aaa	ggc tgg ggt	tgg ctg gcc	ctg ctt ctg	ggg	229
	Met Lys Gly Trp	Gly Trp Leu	Ala Leu Leu	Leu Gly		
	-20	-15	-10			
gcc ctg ctg	gga acc gcc	tgg gct cgg	agg agc cgg	gat ctc cac	tgt	277
Ala Leu Leu	Gly Thr Ala	Trp Ala Arg	Arg Ser Arg	Asp Leu His	Cys	
	-5	1	5			
gga gca tgc	agg gct ctg	gtg gat gaa	cta gaa tgg	gaa att gcc	cag	325
Gly Ala Cys	Arg Ala Leu	Val Asp Glu	Leu Glu Trp	Glu Ile Ala	Gln	
	10	15	20			
gtg gac ccc	aag aag acc	att cag atg	gga tcc ttc	cgg atc aat	cca	373
Val Asp Pro	Lys Lys Thr	Ile Gln Met	Gly Ser Phe	Arg Ile Asn	Pro	
25	30	35	40			
gat ggc agc	cag tca gtg	gtg gag gta	act gtt act	gkt tcc ccc	aaa	421
Asp Gly Ser	Gln Ser Val	Val Glu Val	Thr Val Thr	Xaa Ser Pro	Lys	
	45	50	55			
aca aaa gta	gct cac tct	ggc ttt tgg	atg aaa att	cga ctg ctt	aaa	469
Thr Lys Val	Ala His Ser	Gly Phe Trp	Met Lys Ile	Arg Leu Leu	Lys	
	60	65	70			
aaa gga cct	tgg tct taatag	aaaaa tgaagra	aaaaa cagactc	caga aaaaaag	att	524
Lys Gly Pro	Trp Ser					
	75					
tbggctctgt	ctcawtttgg	aagaaggctg	gcaggcttat	tccccaatgc	aactttgctt	584
cctggctgca	aaccyttaat	acytttgttt	ctgctgtaga	aatttgtag	ccaaaacawg	644
ggagtcctga	twcagcaacc	ccttcttcca	caatccacca	tgactgggtt	ttaatgtamc	704
acttggggta	tacatgcaaa	accatccgtt	cmaaaatctg	aatyccggagc	ttaaaaattt	764
aaaaatgaaa	aacchaaaaa	aaaaaaaa				792

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aggtggagcg accccattac gctaaag atg aaa ggc tgg ggt tgg ctg gcc ctg      174
                               Met Lys Gly Trp Gly Trp Leu Ala Leu
                               -20                               -15
ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat      222
Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
-10                               -5                               1                               5
ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa act aga atg gga      270
Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Thr Arg Met Gly
                               10                               15                               20
aat tgc cca ggt gga ccc caa gaa gac cat tca gat ggg atc ttt ccg      318
Asn Cys Pro Gly Gly Pro Gln Glu Asp His Ser Asp Gly Ile Phe Pro
                               25                               30                               35
gat caa tcc aga tgg cag cca gtc agt ggt gga ggt gcc tta tgc ccg      366
Asp Gln Ser Arg Trp Gln Pro Val Ser Gly Gly Gly Ala Leu Cys Pro
                               40                               45                               50
ctc aga ggc cca cct cac aga gct gct gga gga gat atg tgaccggatg      415
Leu Arg Gly Pro Pro His Arg Ala Ala Gly Gly Asp Met
                               55                               60                               65
aaggagtatg gggaacagat tgatccttcc acccatcgca agaactacgt acgtgtagtg      475
ggccggaatg gagaatccag tgaactggac ctacaaggca tccgaatcga ctcagatatt      535
agcggcaccc tcaagbtttg cgtgtgggaa cattgtggag gaatacgagg atgaactcat      595
tgaattcttt tcccagagag ctgacaatgt taaagacaaa ctttgcagta agcgaacaga      655
tctttgtgac catgccctgc acatatcggc atgatgagct atgaaccact ggagcagccc      715
acactggctt gatggatcac cccaggnaa gggaaaatgg tggcaatgcc ttttatatat      775
tatgttttac tgaaattaac tgaaaaatat gaaacaaaaa gtscaaaaaa aaaaaaa      832

```

<210> 65
<211> 721
<212> DNA
<213> Homo sapiens

<220>

<221> sig_peptide
<222> 156..230
<223> Von Heijne matrix
score 5
seq MFAASLLAMCAGA/EV

<221> polyA_signal
<222> 706..711

<221> polyA_site
<222> 709..721

<221> misc_feature
<222> 351..688
<223> homology
id :H98648
est

<221> misc_feature
<222> 289..353
<223> homology
id :H98648
est

<221> misc_feature
<222> 274..641
<223> homology
id :AA181022
est

<221> misc_feature
<222> 255..286
<223> homology
id :AA181022
est

<221> misc_feature
<222> 242..641
<223> homology
id :AA143192
est

<221> misc_feature
<222> 261..646
<223> homology
id :AA594850
est

<221> misc_feature
<222> 165..474
<223> homology
id :AA563681
est

<221> misc_feature
<222> 1..74
<223> homology
id :AA563681

est

<221> misc_feature
<222> 261..643
<223> homology
id :AA287457
est

<221> misc_feature
<222> 352..646
<223> homology
id :N22567
est

<221> misc_feature
<222> 299..354
<223> homology
id :N22567
est

<221> misc_feature
<222> 265..303
<223> homology
id :N22567
est

<221> misc_feature
<222> 30..165
<223> homology
id :AA186657
est

<221> misc_feature
<222> 270..349
<223> homology
id :AA186657
est

<221> misc_feature
<222> 213..261
<223> homology
id :AA186657
est

<221> misc_feature
<222> 165..214
<223> homology
id :AA186657
est

<221> misc_feature
<222> 346..387
<223> homology
id :AA186657
est

<221> misc_feature
<222> 52..400

<223> homology
 id :HSC1ED081
 est

<221> misc_feature
 <222> 398..436
 <223> homology
 id :HSC1ED081
 est

<221> misc_feature
 <222> 171..316
 <223> homology
 id :AA143136
 est

<400> 65
 attttgggtc cggcctgctc gcmgtccgct ccgtccgccc ttagacctgt tgcccagcat 60
 ccctgcagtt cgcggwacag tctctattag agcgcgtgta tagaggcaga kaggagtga 120
 gtccacagtt cctctcctcc tagagcctgc cgacc atg ccc gcg ggc gtg ccc 173
 Met Pro Ala Gly Val Pro
 -25 -20
 atg tcc acc tac ctg aaa atg ttc gca gcc agt ctc ctg gcc atg tgc 221
 Met Ser Thr Tyr Leu Lys Met Phe Ala Ala Ser Leu Leu Ala Met Cys
 -15 -10 -5
 gca ggg gca gaa gtg gtg cac agg tac tac cga ccg gac ctg aca ata 269
 Ala Gly Ala Glu Val Val His Arg Tyr Tyr Arg Pro Asp Leu Thr Ile
 1 5 10
 cct gaa att cca cca aag cgt gga gaa ctc aaa acg gag ctt ttg gga 317
 Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu Lys Thr Glu Leu Leu Gly
 15 20 25
 ctg aaa gaa aga aaa cac aaa cct caa gtt tct caa cag gag gaa ctt 365
 Leu Lys Glu Arg Lys His Lys Pro Gln Val Ser Gln Gln Glu Glu Leu
 30 35 40 45
 aaa taactatgcc aagaattctg tgaataatat aagtcttaaa tatgtatttc 418
 Lys
 ttaatttatt gcatcaaact acttgtcctt aagcacttag tctaattgcta actgcaagag 478
 gaggtgctca gtggatgttt agccgatacg ttgaaattta attacggttt gattgatatt 538
 tcttgaaaac tgccaaagca catatcatca aaccatttca tgaatatggt ttggaagatg 598
 tttagtcttg aatataacgc gaaatagaat atttgtaagt ctactatatg gggtgtcttt 658
 atttcatata aattaagaaa ttattttaaa actatgaact aggtttcatt aaaaaaaaaa 718
 gaa 721

<210> 66
 <211> 531
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 272..397
 <223> Von Heijne matrix
 score 4.599999990463257
 seq RIPSLPGSPVCWA/WP

<221> polyA_signal
 <222> 503..508

<221> polyA_site
<222> 518..531

<221> misc_feature
<222> 235..517
<223> homology
id :AA524403
est

<221> misc_feature
<222> 52..208
<223> homology
id :AA524403
est

<221> misc_feature
<222> 259..517
<223> homology
id :N93600
est

<221> misc_feature
<222> 85..207
<223> homology
id :N93600
est

<221> misc_feature
<222> 353..517
<223> homology
id :AA594610
est

<221> misc_feature
<222> 258..363
<223> homology
id :AA594610
est

<221> misc_feature
<222> 105..207
<223> homology
id :AA594610
est

<221> misc_feature
<222> 202..517
<223> homology
id :AA074748
est

<221> misc_feature
<222> 116..153
<223> homology
id :AA074748
est

<221> misc_feature
<222> 167..202
<223> homology
id :AA074748
est

<221> misc_feature
<222> 258..517
<223> homology
id :N93603
est

<221> misc_feature
<222> 208..251
<223> homology
id :N93603
est

<221> misc_feature
<222> 163..202
<223> homology
id :N93603
est

<221> misc_feature
<222> 90..125
<223> homology
id :N93603
est

<221> misc_feature
<222> 125..363
<223> homology
id :HSPD04938
est

<221> misc_feature
<222> 353..517
<223> homology
id :HSPD04938
est

<221> misc_feature
<222> 28..227
<223> homology
id :AA074804
est

<221> misc_feature
<222> 265..310
<223> homology
id :AA074804
est

<221> misc_feature
<222> 227..263
<223> homology
id :AA074804

est

<221> misc_feature
<222> 352..385
<223> homology
id :AA074804
est

<400> 66

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aaaaggaaag aggtysggag cgctcgcgag atctcggacc acccaacctg aaaggtgctt      60
aggaagtga aaggccaga ggaggcctcc gggcaaattg ccggagctgg accgacctg      120
ctgctacgag aagagaatgg ctgttgagct cggcgtcaga gcagctccag tgccggggat      180
tcggacggag agcgcgagga ctggcgggct gaggcgcccc gacagcagct agaggcgctg      240
ctcaacaaga ctatgcgcat tcgcatgaca g atg gac gga cac tgg tcg gct      292
```

Met Asp Gly His Trp Ser Ala

-40

```
gct ttc tct gca ctg acc gtg act gca atg tca tcc tgg gct cgg cgc      340
Ala Phe Ser Ala Leu Thr Val Thr Ala Met Ser Ser Trp Ala Arg Arg
-35 -30 -25 -20
```

```
agg agt tcc tca agc cgt cgg att cct tct ctg ccg ggg agc ccc gtg      388
Arg Ser Ser Ser Ser Arg Arg Ile Pro Ser Leu Pro Gly Ser Pro Val
-15 -10 -5
```

```
ttgc tgg gcc tgg cca tgg tac ccg gac acc aca tcg ttt cca ttg agg      436
Cys Trp Ala Trp Pro Trp Tyr Pro Asp Thr Thr Ser Phe Pro Leu Arg
1 5 10
```

```
ttgc aga ggg aga gtc tgaccgggcc tccgtatctc tgaccacgat ggcgcttacc      491
Cys Arg Gly Arg Val
15
```

```
tttcagactt cattaaactt atgaccaaaa aaaaaaaaaa      531
```

<210> 67
<211> 783
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 381..629
<223> Von Heijne matrix
score 8.60000038146973
seq LELLTSCSPPASA/SQ

<221> polyA_signal
<222> 736..741

<221> polyA_site
<222> 770..783

<221> misc_feature
<222> 207..263
<223> homology
id :AA357230
est

<400> 67

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agggacttcc ggctcgcgtg gcgtggacgt ttgtgggtggg gcgtgttggt ccgcgctctc      60
agaactgtgc tgggaaggat ggtagggcga ctggggctca cctccgcacc gttgtaggac      120
```



```

ccggggtagg gttttgagcc cgtgggagct gccccacgcg gcctcgtcct gccaacggtc 180
ggatggcgga gacgaaggac gcagcgaga tggtggtgac cttcaaggat gtggctgtga 240
cctttacccg ggaggagtgg agacagctgg acctggccca gaggaccctg taccgagagg 300
tgatcgggtt cccaaaccag agttggtcca cctgctagag catgggcagg agctgtggat 360
agtgaagaga ggcctctcac atg cta cct gtg cag agt ttc act ctt gtt gcc 413
                               Met Leu Pro Val Gln Ser Phe Thr Leu Val Ala
                               -80                               -75
cag gct gga gtg cag tgg cgc cat ctc agc tca ctg caa ctt ctg cct 461
Gln Ala Gly Val Gln Trp Arg His Leu Ser Ser Leu Gln Leu Leu Pro
-70                               -65                               -60
ccc gag ttc aag gga ttc tcc tgc ctc agc ctc ccg agt agc tgg gat 509
Pro Glu Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp
-55                               -50                               -45
tac agg cgc cca cca cca tgc ccg gct ggt ttt ttt gta ttt tta gta 557
Tyr Arg Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val
-40                               -35                               -30                               -25
gag acg ggg ctt cac cat gtt ggc cag gct ggt ctt gaa ctc ttg acc 605
Glu Thr Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr
-20                               -15                               -10
tca tgt agt cca ccc gcc tct gcc tcc caa agt gct gcg att aca ggc 653
Ser Cys Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly
-5                               1                               5
gtg agc cac gtg ccc ggc aaa aaa aaa ctg ctt aag gtt gaa aag aaa 701
Val Ser His Val Pro Gly Lys Lys Lys Leu Leu Lys Val Glu Lys Lys
10                               15                               20
aat tta aga aaw ttg ctg acg gra ata aaa acy taataaaaact accacccgaa 754
Asn Leu Arg Xaa Leu Thr Xaa Ile Lys Thr
25                               30                               35
ggaatgaaaa aaccataaaaa aaaaaaaaaa 783

```

```

<210> 68
<211> 996
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> sig_peptide
<222> 140..205
<223> Von Heijne matrix
      score 5.90000009536743
      seq IILGCLALFLLLQ/RK

```

```

<221> polyA_signal
<222> 965..970

```

```

<221> polyA_site
<222> 984..996

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```

<221> misc_feature
<222> 676..959
<223> homology
      id :AA399103
      est

```

```

<221> misc_feature
<222> 609..679
<223> homology

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id :AA399103
est

<221> misc_feature
<222> 225..433
<223> homology
id :AA398040
est

<221> misc_feature
<222> 433..563
<223> homology
id :AA398040
est

<400> 68

aacagttacg aaggagagct gcaaaagttg cagcagaaag gttgggagtc cgcacaggtt 60
ccgtagccca cagaaaagaa gcaaggagcg gcaggactgt ttcacacttt tctgcttctg 120
gaagggtgctg gacaaaaac atg gaa cta att tcc cca aca gtg att ata atc 172
Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile

-20

-15

ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat ttg cgc 220
Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg
-10 -5 1 5

aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt gga ttt 268
Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe
10 15 20

gak ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga atc aag 316
Xaa Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys
25 30 35

gta tgt ggt cgt ggc ava cgg ggt ctc cag agg aga caa tgc ttt ctt 364
Val Cys Gly Arg Gly Xaa Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu
40 45 50

ttt taaactttct ttcattgact cttaagtga gggctagaac acggggaaca 417
Phe

tacctgcttg cctcaaaacta aaggatctag tcmtytctga aktcctctac tsacrtrtra 477
caacaatatt ctgtgcaaaa ttttgcaaaa gaaatgaaat acaattgcmg cgtgcatcga 537
catttttgga agtagagatt aacyttcgt atttttactt cmtcgaagtt aagttccaaa 597
tgtgtatgtg ttaagtaaat gttttcagta aytgggaaag ataaagtgt atccaattta 657
agtttgtgaa aatgagtaat tccgtatcca aaytggagtt aacaccaaag tattgtacaa 717
attgcttgca cagttggtcc gtacacaata gacaggctyt gtatttttag ctgacgttgt 777
tatttgatga tgatgtactc cattttcamt acggcccga gagamtagta atcctccttg 837
tagtagatgt ttttgtcttg aaagtatctt ttaaagtgt gagcacttta aggaacagac 897
ccttattaat gtyttttaag ttttattcaa tttccagtca caaatatttt atggtatttg 957
attgtytaat aaatttgtat gatattaaaa aaaaaaaaa 996

<210> 69
<211> 657
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 183..338
<223> Von Heijne matrix
score 3.79999995231628
seq VMLETGGLLVSLG/QS

<221> polyA_signal
<222> 620..625

<221> polyA_site
<222> 644..657

<221> misc_feature
<222> 207..263
<223> homology
id :AA357230
est

<400> 69
agggacttcc ggcctcgctg gcgtggacgt ttgtggtggg gcgtgttggt ccgcgctctc 60
agaactgtgc tgggaaggat ggtagggcga ctggggctca cctccgcacc gttgtaggac 120
ccggggtagg gttttgagcc cgtgggagct gccccacgcg gcctcgtcct gccaacggtc 180
gg atg gcg gag acg aag gac gca gcg cag atg ttg gtg acc ttc aag 227
Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys
-50 -45 -40
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg 275
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
-35 -30 -25
gcc cag agg acc ctg tac cga gag gtg atg ctg gag acc tgt ggg ctt 323
Ala Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu
-20 -15 -10
ctg gtt tca cta ggg caa agc att tgg ctg cat ata aca gaa aac cag 371
Leu Val Ser Leu Gly Gln Ser Ile Trp Leu His Ile Thr Glu Asn Gln
-5 1 5 10
atc aaa ctg gct tca cct gga agg aaa ttc act aac tcg cct gat gag 419
Ile Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu
15 20 25
aag cct gag gtg tgg ttg gct cca ggc ctg ttc ggt gcc gca gcc cag 467
Lys Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln
30 35 40
tgacgccatc aaggatgtct tggttctctg ttccttcttc ttggttcagg cttctggatt 527
gtcctcaggc tggctcctca tagggatgct ggggtctgca gccttgactg gggcagcagg 587
cccccatggt tcaatccatc ctcccacctt ggaataaatg ctttcttttc acaatgagaa 647
aaaaaaaaaa 657

<210> 70
<211> 416
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 140..205
<223> Von Heijne matrix
score 5.90000009536743
seq IILGCLALFLLLQ/RK

<221> polyA_signal
<222> 383..388

<221> polyA_site
<222> 405..416

<221> misc_feature
 <222> 225..316
 <223> homology
 id :AA398040
 est

<400> 70

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aacagttacg aaggagagct gcaaaagttg cagcagaaaag gttgggagtc cgcacaggtt      60
ccgtagccca cagaaaagaa gcaagggacg gcaggactgt ttcacacttt tctgcttctg      120
gaaggtgctg gacaaaaaac atg gaa cta att tcc cca aca gtg att ata atc      172
                Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile
                -20                                -15

ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat ttg cgc      220
Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg
   -10                                -5                                1                                5
aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt gga ttt      268
Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe
                10                                15                                20

gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga atc aag      316
Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys
                25                                30                                35

tat gga cca ata ttt aca gtc ttt gct atg gga aac cga atg acc ttt      364
Tyr Gly Pro Ile Phe Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe
   40                                45                                50

gtt act gaa gaa gga agg aat taatgtgttt ctaaaatcca aaaaaaaaaa a      416
Val Thr Glu Glu Gly Arg Asn
   55                                60

```

<210> 71

<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 129..176

<223> Von Heijne matrix
 score 4.80000019073486
 seq SLFIYIFLTCSNT/SP

<221> polyA_signal

<222> 513..518

<221> polyA_site

<222> 530..543

<221> misc_feature

<222> 264..500

<223> homology
 id :AA534039
 est

<221> misc_feature

<222> 205..315

<223> homology
 id :T82645

est

<221> misc_feature
<222> 295..382
<223> homology
id :T82645
est

<221> misc_feature
<222> 375..405
<223> homology
id :T82645
est

<400> 71

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actgtcccat tcctcccct acaacacaca cacctttcag gcagggasgn gatgagcttc      60
cagccccaag agtggaggct gccacatcct aacatasgta tctattgaaa aggaagcagt      120
gtgtatct atg att ata tct ctg ttc atc tat ata ttt ttg aca tgt agc      170
      Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser
      -15 -10 -5
aac acc tct cca tct tat caa gga act caa ctc ggt ctg ggt ctc ccc      218
Asn Thr Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro
      1 5 10
agt gcc cag tgg tgg cct ttg aca ggt agg agg atg cag tgc tgc agg      266
Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg
      15 20 25 30
cta ttt tgt ttt ttg tta caa aac tgt ctt ttc cct ttt ccc ctc cac      314
Leu Phe Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His
      35 40 45
ctg att cag cat gat ccc tgt gag ctg gtt ctc aca atc tcc tgg gac      362
Leu Ile Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp
      50 55 60
tgg gct gag gca ggg gct tcg ctc tat tct ccc taaccatact gtcttccttt      415
Trp Ala Glu Ala Gly Ala Ser Leu Tyr Ser Pro
      65 70
cccccttgcc acttagcagt tatccccca gctatgcctt ctccctccct cccttgccct      475
ggcatatatt gtgccttatt tatgctgcaa atataacatt aaactatcaa gtgaaaaaaa      535
aaaaaaaaa      543
```

<210> 72
<211> 605
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 285..341
<223> Von Heijne matrix
score 5.59999990463257
seq PTLCVSSSPALWA/AS

<221> polyA_signal
<222> 575..580

<221> polyA_site
<222> 592..605

```

<221> misc_feature
<222> 53..296
<223> homology
      id :W07033
      est

<221> misc_feature
<222> 348..432
<223> homology
      id :W07033
      est

<221> misc_feature
<222> 435..497
<223> homology
      id :W07033
      est

<221> misc_feature
<222> 293..337
<223> homology
      id :W07033
      est

<221> misc_feature
<222> 521..560
<223> homology
      id :W07033
      est

<221> misc_feature
<222> 489..520
<223> homology
      id :W07033
      est

<221> misc_feature
<222> 15..337
<223> homology
      id :AA151004
      est

<221> misc_feature
<222> 348..412
<223> homology
      id :AA151004
      est

<221> misc_feature
<222> 434..485
<223> homology
      id :AA151004
      est

<221> misc_feature
<222> 83..324
<223> homology
      id :AA476506

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est

<221> misc_feature
<222> 347..560
<223> homology
id :AA476506
est

<221> misc_feature
<222> 16..347
<223> homology
id :W56567
est

<221> misc_feature
<222> 350..405
<223> homology
id :W56567
est

<221> misc_feature
<222> 433..470
<223> homology
id :W56567
est

<221> misc_feature
<222> 15..296
<223> homology
id :AA147584
est

<221> misc_feature
<222> 348..421
<223> homology
id :AA147584
est

<221> misc_feature
<222> 293..337
<223> homology
id :AA147584
est

<221> misc_feature
<222> 419..453
<223> homology
id :AA147584
est

<221> misc_feature
<222> 2..338
<223> homology
id :AA281959
est

<221> misc_feature
<222> 350..432

<223> homology
 id :AA281959
 est

<400> 72
 aacgcctwta agacagcgga actaagaaaa gaagaggcct gtggacagaa caatcatgtc 60
 tgactccctg gtggtgtgcg aggtagaccc agagctaaca gaaaagctga kgaaattccg 120
 cttccgaaaa gagacagaca atgcagccat cataatgaag gtggacaaag accggcagat 180
 ggtggtgctg gaggaagaat ttcagaacat ttcccagag gagtcaaaa tggagttgcc 240
 ggagagacag cccaggttcg tggtttacag ctacaagtac gtgc atg acg atg gcc 296
 Met Thr Met Ala
 gag tgt cct acc ctt tgt gtt tca tct tct cca gcc ctg tgg gct gca 344
 Glu Cys Pro Thr Leu Cys Val Ser Ser Ser Pro Ala Leu Trp Ala Ala
 -15 -10 -5 1
 agc gaa aca aca gat gat gta tgc agg gag taaaaacagg ctggtgcaga 394
 Ser Glu Thr Thr Asp Asp Val Cys Arg Glu
 5 10
 cagcagagct cacaaagggtg ttcgaaatcc gcaccactga tgacctcact gaggcctggc 454
 tccaagaaaa gttgtctttc tttcgttgat ctctgggctg gggactgaat tcctgatgtc 514
 tgagtctca aggtgactgg ggacttgaa cccctaggac ctgaacaacc aaggacttta 574
 aataaatttt aaaatgcaaa aaaaaaaaaa a 605

<210> 73
 <211> 864
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 136..444
 <223> Von Heijne matrix
 score 4.90000009536743
 seq VYAFLGLTAPSGS/KE

<221> polyA_signal
 <222> 835..840
 <221> polyA_site
 <222> 851..864

<221> misc_feature
 <222> 222..456
 <223> homology
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<221> misc_feature
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<223> homology
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<221> misc_feature
<222> 222..458
<223> homology

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<221> misc_feature
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<221> misc_feature
<222> 130..419
<223> homology
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<221> misc_feature
<222> 59..130
<223> homology
id :T35647
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<221> misc_feature
<222> 557..852
<223> homology
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<221> misc_feature
<222> 501..571
<223> homology
id :HUM093F06A
est

<221> misc_feature
<222> 130..384
<223> homology
id :T35666
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<400> 73
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ggattccagc cattgctgca gctgctccac agcccttttc aggacccaaa caaccgcagc 120
cgctgttccc caggr atg gtg atc cgt gta tat att gca tct tcc tct ggc 171
Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly
-100 -95
tct aca gcg att aag aag aaa caa caa gat gtg ctt ggt ttc cta gaa 219
Ser Thr Ala Ile Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu
-90 -85 -80
gcc aac aaa ata gga ttt gaa gaa aaa gat att gca gcc aat gaa gag 267
Ala Asn Lys Ile Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu
-75 -70 -65 -60
aat cgg aag tgg atg aga gaa aat gta cct gaa aat agt cga cca gcc 315

Asn Arg Lys Trp Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala	
-55 -50 -45	
aca ggt aac ccc ctg cca cct cag att ttc aat gaa agc cag tat cgc	363
Thr Gly Asn Pro Leu Pro Pro Gln Ile Phe Asn Glu Ser Gln Tyr Arg	
-40 -35 -30	
ggg gac tat gat gcc ttc ttt gaa gcc aga gaa aat aat gca gtg tat	411
Gly Asp Tyr Asp Ala Phe Phe Glu Ala Arg Glu Asn Ala Val Tyr	
-25 -20 -15	
gcc ttc tta ggc ttg aca gcc cca tct ggt tca aag gaa gca gga agg	459
Ala Phe Leu Gly Leu Thr Ala Pro Ser Gly Ser Lys Glu Ala Gly Arg	
-10 -5 1 5	
tgc aag caa agc agc aag cca tgaaccttga gcaactgtgct tttaagcatc	510
Cys Lys Gln Ser Ser Lys Pro	
10	
ctgaaaaatg agtctccatt gcttttataa aatagcagaa ttagctttgc sttcaaaaga	570
aataggstta atgttgaaat aatagattag ttgggttttc acatgcaaac amtcaaaatg	630
aatacaaaat taaaatttga acattatggt gattatggtg aggagaatgg gatattaaca	690
taaaattata ttaataagta gatatygtag aaatagtgtt gttacctgcc aagccatcct	750
gtatacacca atgattttac aaagaaaaca cccttccttc cttytgccat tamtatggca	810
acctaagtgt atytgcagct ttacattaaa aaggagaaaag agaaaaaaaa aaaa	864

<210> 74
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 <212> DNA
 <213> Homo sapiens

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 <222> 200..427
 <223> Von Heijne matrix
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<221> polyA_signal
 <222> 1001..1006
 <221> polyA_site
 <222> 1022..1033

<221> misc_feature
 <222> 55..406
 <223> homology
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<221> misc_feature
 <222> 397..487
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 id :AA056667
 est

<221> misc_feature
 <222> 527..584
 <223> homology
 id :AA056667
 est

<221> misc_feature
<222> 482..531
<223> homology
id :AA056667
est

<221> misc_feature
<222> 581..634
<223> homology
id :AA056667
est

<221> misc_feature
<222> 397..700
<223> homology
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<221> misc_feature
<222> 222..406
<223> homology
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<221> misc_feature
<222> 693..748
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id :AA044187
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<221> misc_feature
<222> 68..406
<223> homology
id :AA131958
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<221> misc_feature
<222> 397..517
<223> homology
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<221> misc_feature
<222> 510..558
<223> homology
id :AA131958
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<221> misc_feature
<222> 77..531
<223> homology
id :W95957
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<221> misc_feature
<222> 527..558
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id :W95957

est

<221> misc_feature
<222> 397..586
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<221> misc_feature
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<223> homology
id :AA041216
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<221> misc_feature
<222> 582..700
<223> homology
id :AA041216
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<221> misc_feature
<222> 77..406
<223> homology
id :W95790
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<221> misc_feature
<222> 397..539
<223> homology
id :W95790
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<221> misc_feature
<222> 474..760
<223> homology
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<221> misc_feature
<222> 788..940
<223> homology
id :AA461134
est

<400> 74

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cctgaagtga	cagcggagag	aaccaggcag	cccagaaacc	ccaggcgtgg	agattgatcc	120
tgcgagagaa	gggggttcat	catggcggat	gacctaaagc	gattcttgta	taaaaagtta	180
ccaagtgttg	aagggtctcc	atg cca ttg ttg tgt cag ata gag atg gag tac				232
		Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr				
		-75	-70			
ctg tta tta aag tgg caa atg aca atg ctc cag agc atg ctt tgc gac						280
Leu Leu Leu Lys Trp Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp						
-65	-60	-55	-50			
ctg gtt tct tat cca ctt ttg ccc ttg caa cag acc aag gaa gca aac						328
Leu Val Ser Tyr Pro Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn						
	-45	-40	-35			
ttg gac ttt cca aaa ata aaa gta tca tct gtt act ata aca cct acc						376

Leu Asp Phe Pro Lys Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr	
-30 -25 -20	
agg tgg ttc aat tta atc gtt tac ctt tgg gtg gtg agt ttc ata gcc	424
Arg Trp Phe Asn Leu Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala	
-15 -10 -5	
agc agc agt gcc aat aca gga cta att gtc agc cta gaa aag gaa ctt	472
Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu	
1 5 10 15	
gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa gtt tct	514
Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser	
20 25	
taatctgaca gtgggtttcag tgtgtacctt atcttcatta taacaacaca atatcaatcc	574
agcaatcttt agactacaat aatactttta tccatgtgct caagaaaggg cccctttttc	634
caacttatac taaagagcta gcatatagat gtaattttata gatagatcag ttgctatatt	694
ttctgggtgta ggggtctttct tatttagtga gatctaggga taccacagaa atgggttcagt	754
ctatcaacag ctcccatgga gttagtctgg tcacagatat ggatgagaga ttttattcag	814
tggatcagaa tcaaactggg acattgatcc acttgagccg ttaagtgtg ccaattgtac	874
aatatgccca ggcttgacaga ataaagccaa cttttttattg tgaataataa taaggacata	934
tttttyttca gattatgttt tatttytttg cattgagtga ggaacataaa atggcttggt	994
aaaagtaata aaatcagtac aatcactaaa aaaaaaaaaa	1033

<210> 75
 <211> 499
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> sig_peptide
 <222> 68..133
 <223> Von Heijne matrix
 score 9.80000019073486
 seq LVVFCLALQLVPG/SP
 <221> polyA_signal
 <222> 472..477
 <221> polyA_site
 <222> 490..499

<400> 75	
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tgacacc atg aag cct gtg ctg cct ctc cag ttc ctg gtg gtg ttc tgc	109
Met Lys Pro Val Leu Pro Leu Gln Phe Leu Val Val Phe Cys	
-20 -15 -10	
cta gca ctg cag ctg gtg cct ggg agt ccc aag cag cgt gtt ctg aag	157
Leu Ala Leu Gln Leu Val Pro Gly Ser Pro Lys Gln Arg Val Leu Lys	
-5 1 5	
tat atc ttg gaa cct cca ccc tgc ata tca gca cct gaa aac tgt act	205
Tyr Ile Leu Glu Pro Pro Cys Ile Ser Ala Pro Glu Asn Cys Thr	
10 15 20	
cac ctg tgt aca atg cag gaa gat tgc gag aaa gga ttt cag tgc tgt	253
His Leu Cys Thr Met Gln Glu Asp Cys Glu Lys Gly Phe Gln Cys Cys	
25 30 35 40	
tcc tcc ttc tgt ggg ata gtc tgt tca tca gaa aca ttt caa aag cgc	301
Ser Ser Phe Cys Gly Ile Val Cys Ser Ser Glu Thr Phe Gln Lys Arg	
45 50 55	
aac aga atc aaa cac aag ggc tca gaa gtc atc atg cct gcc aac	346

Asn Arg Ile Lys His Lys Gly Ser Glu Val Ile Met Pro Ala Asn	
60 65 70	
tgaggcatat ttcctagatc attttgcctc tacgatgttt tttcttggtc cacctttagg	406
aaggatttga gaagcaagaa actggaggcc caatatctaa cctgcaaadc gtttttgagt	466
ttggcaataa aggcataatc accaaaaaaaa aaa	499

<210> 76
 <211> 978
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 274..399
 <223> Von Heijne matrix
 score 5.19999980926514
 seq LLFDLVCHEFCQS/DD

<221> polyA_signal
 <222> 943..948

<221> polyA_site
 <222> 966..978
 <221> misc_feature
 <222> 335..518
 <223> homology
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<221> misc_feature
 <222> 225..274
 <223> homology
 id :AA206225
 est

<221> misc_feature
 <222> 812..861
 <223> homology
 id :AA206225
 est

<221> misc_feature
 <222> 186..224
 <223> homology
 id :AA206225
 est

<221> misc_feature
 <222> 708..748
 <223> homology
 id :AA206225
 est

<221> misc_feature
 <222> 276..314
 <223> homology

id :AA206225
est

<221> misc_feature
<222> 146..176
<223> homology
id :AA206225
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<221> misc_feature
<222> 879..909
<223> homology
id :AA206225
est

<221> misc_feature
<222> 182..518
<223> homology
id :C15003
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<221> misc_feature
<222> 708..748
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<221> misc_feature
<222> 182..517
<223> homology
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est

<221> misc_feature
<222> 170..202
<223> homology
id :AA544037
est

<221> misc_feature
<222> 517..595
<223> homology
id :HUM00TW170
est

<221> misc_feature
<222> 596..665
<223> homology
id :HUM00TW170
est

<221> misc_feature
<222> 697..748
<223> homology
id :HUM00TW170
est

<221> misc_feature

<222> 805..861
 <223> homology
 id :HUM00TW170
 est

<221> misc_feature
 <222> 212..369
 <223> homology
 id :HUM169E08B
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<221> misc_feature
 <222> 406..493
 <223> homology
 id :HUM169E08B
 est

<221> misc_feature
 <222> 542..595
 <223> homology
 id :HUM00TW112
 est

<221> misc_feature
 <222> 697..748
 <223> homology
 id :HUM00TW112
 est

<400> 76

accaggaaca tccagctatt tatgatagca tttgcttcat tatgtcaagt tcaacaaatg	60
ttgacttgct ggtgaagggtg ggggagggtg tggacaagct ctttgatttg gatgagaaac	120
taatgttaag aatgggtcag aaatggggct gctcagcctc tggaccaacc ccaggaagag	180
tctgaagagc agccagtgtt tcggcttggt cccgtgtatac ttgaagctgc caaacaagta	240
cgttctgaaa atccagaatg gcttgatggt tac atg cac att tta caa ctg ctt	294
Met His Ile Leu Gln Leu Leu	

-40

act aca gtg gat gat gga att caa gca att gta cat tgt cct gac act	342
Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His Cys Pro Asp Thr	
-35 -30 -25 -20	

gga aaa gac att tgg aat tta ctt ttt gac ctg gtc tgc cat gaa ttc	390
Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val Cys His Glu Phe	
-15 -10 -5	

tgc cag tct gat gat cca gcc atc att ctt caa gaa cag aaa aca gtg	438
Cys Gln Ser Asp Asp Pro Ala Ile Ile Leu Gln Glu Gln Lys Thr Val	
1 5 10	

cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat gcc tca cag act	486
Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr Ala Ser Gln Thr	
15 20 25	

gag caa gag tat cta aag ata gaa aaa gta gat ctt cct cta att gac	534
Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val Asp Leu Pro Leu Ile Asp	
30 35 40 45	

agc ctc att cgg gtc tta caa aat atg gaa cag tgt cag aaa aaa cca	582
Ser Leu Ile Arg Val Leu Gln Asn Met Glu Gln Cys Gln Lys Lys Pro	
50 55 60	

gag aac tcg gca gga gtc taacacagag gaaactaaaa ggactgattt	630
Glu Asn Ser Ala Gly Val	
65	

aacccaagat	gatttccact	tgaaaatctt	aaaaggatat	tgttatggtg	aagtttctgt	690
ctaataattt	ttcaggcatt	aacaaaggag	acggtggctc	agggagtaaa	ggaaggccgt	750
tgagcaaaca	gaagtgttcc	tctgcaattt	caaaarcctt	cttctttcta	tagcccctgt	810
gggtggaaga	ttttattaaa	atcctacgtg	aagttgataa	ggcgcttgct	kgatgacttg	870
gaaaaaaamc	ttccaagtt	tgaaggttca	gaastaaaaa	rscktgaatg	ggaattactt	930
sstgtbcaag	aaaataaact	ttatTTTTct	cactgaaaaa	aaaaaaa		978

<210> 77
 <211> 587
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 421..465
 <223> Von Heijne matrix
 score 3.90000009536743
 seq LVPLGQSFPLSEP/RC

<221> polyA_signal
 <222> 553..558

<221> polyA_site
 <222> 575..587
 <221> misc_feature
 <222> 182..322
 <223> homology
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 est

<221> misc_feature
 <222> 32..132
 <223> homology
 id :T35951
 est

<221> misc_feature
 <222> 136..193
 <223> homology
 id :T35951
 est

<221> misc_feature
 <222> 182..322
 <223> homology
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<221> misc_feature
 <222> 32..132
 <223> homology
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<221> misc_feature
 <222> 136..193

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<223> homology
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<221> misc_feature
<222> 136..299
<223> homology
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<221> misc_feature
<222> 32..132
<223> homology
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    est

<221> misc_feature
<222> 136..322
<223> homology
    id :AA381001
    est

<221> misc_feature
<222> 85..132
<223> homology
    id :AA381001
    est

<221> misc_feature
<222> 182..322
<223> homology
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    est

<221> misc_feature
<222> 136..193
<223> homology
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    est

<221> misc_feature
<222> 82..132
<223> homology
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    est

<221> misc_feature
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<223> homology
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<221> misc_feature
<222> 475..554
<223> homology
    id :AA477628
    est

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<221> misc_feature
 <222> 182..322
 <223> homology
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 est

<221> misc_feature
 <222> 136..192
 <223> homology
 id :HSC34G011
 est

<221> misc_feature
 <222> 41..119
 <223> homology
 id :AA090647
 est

<221> misc_feature
 <222> 136..184
 <223> homology
 id :AA090647
 est

<221> misc_feature
 <222> 316..426
 <223> homology
 id :AA505962
 est

<400> 77

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gaaaccagaa	gaaaaatatg	agacggggaa	tcacgtgtg	atgtgtgtgc	tgcccttggc	120
tkwgtgtgk	gaagtycckg	ctcaggtggt	aggtacagt	tggttgatcg	tggtggcttg	180
aggggaaccc	gctgttcaga	gctgtgactg	cggctgcact	cagagaagct	gcccttggct	240
gctcgtagcg	ccgggccttc	tctcctcgtc	atcatccaga	gcagccagt	tccgggaggc	300
agaagatgcc	ccactccagc	ctctggactg	ggggctctct	tcagtggctg	aatgtccagc	360
agagctattt	ccttccacag	ggggccttgc	aggggaagggt	ccaggacttg	acatcttaag	420
atg cgt ctt gtc ccc ttg ggc cag tca ttt ccc ctc tct gag cct cgg						468
Met Arg Leu Val Pro Leu Gly Gln Ser Phe Pro Leu Ser Glu Pro Arg						
-15	-10	-5	1			
tgt ctt caa cct gtg aaa tgg gat cat aat cac tgc ctt acc tcc ctc						516
Cys Leu Gln Pro Val Lys Trp Asp His Asn His Cys Leu Thr Ser Leu						
5	10	15				
acg gtt gtt gtg agg act gag tgt gtg gaa gtt ttt cat aaa ctt tgg						564
Thr Val Val Val Arg Thr Glu Cys Val Glu Val Phe His Lys Leu Trp						
20	25	30				
atg cta gtg taaaaaaaaa aaaa						587
Met Leu Val						
35						

<210> 78
 <211> 400
 <212> DNA
 <213> Homo sapiens

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<221> sig_peptide
 <222> 198..278
 <223> Von Heijne matrix
 score 4.90000009536743
 seq CLLSYIALGAIHA/KI

<221> polyA_signal
 <222> 364..369

<221> polyA_site
 <222> 387..400

<400> 78
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 tctgactcca tggaaaccag atggggcaac ggggtggttc tagtgcagac tgtagctgca 120
 gtcctctcc acctctagcc tgctcatttc cagctcagaa attctactaa tggcggtttt 180
 tcttctgaa aaaggaa atg aac agg gtc cct gct gat tct cca aat atg 230
 Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met
 -25 -20
 tgt cta atc tgt tta ctg agt tac ata gca ctt gga gcc atc cat gca 278
 Cys Leu Ile Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala
 -15 -10 -5
 aaa atc tgt aga aga gca ttc cag gaa gag gga aga gca aat gca aag 326
 Lys Ile Cys Arg Arg Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys
 1 5 10 15
 acg ggc gtg aga gct tgg tgc ata cag cca tgg gcc aaa taaagtttcc 375
 Thr Gly Val Arg Ala Trp Cys Ile Gln Pro Trp Ala Lys
 20 25
 ttggaatagc caaaaaaaaa aaaaa 400

<210> 79
 <211> 1166
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 167..229
 <223> Von Heijne matrix
 score 5.59999990463257
 seq LVLSLQFLLSYD/LF

<221> polyA_signal
 <222> 1133..1138

<221> polyA_site
 <222> 1154..1166

<221> misc_feature
 <222> 22..377
 <223> homology
 id :AA306911
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<221> misc_feature
 <222> 424..540
 <223> homology

id :AA306911
est

<221> misc_feature
<222> 376..424
<223> homology
id :AA306911
est

<221> misc_feature
<222> 4..458
<223> homology
id :AA417777
est

<221> misc_feature
<222> 10..447
<223> homology
id :AA236327
est

<221> misc_feature
<222> 279..714
<223> homology
id :AA410332
est

<221> misc_feature
<222> 680..893
<223> homology
id :N32991
est

<221> misc_feature
<222> 881..1023
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<221> misc_feature
<222> 1056..1109
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id :N32991
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<221> misc_feature
<222> 1122..1153
<223> homology
id :N32991
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<221> misc_feature
<222> 1024..1054
<223> homology
id :N32991
est

<221> misc_feature

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	acc	agt	aac	tac	agc	ctg	gtg	ctc	tct	ctg	cag	ttc	ctg	ctg	ctg	tcc	223
	Thr	Ser	Asn	Tyr	Ser	Leu	Val	Leu	Ser	Leu	Gln	Phe	Leu	Leu	Leu	Ser	
			-15						-10					-5			
	tat	gac	ctc	ttt	gtc	aat	tcc	ttc	tca	gaa	ctg	ctc	caa	aag	act	cct	271
	Tyr	Asp	Leu	Phe	Val	Asn	Ser	Phe	Ser	Glu	Leu	Leu	Gln	Lys	Thr	Pro	
			1				5					10					
	gtc	atc	cag	ctt	gtg	ctc	ttc	atc	atc	cag	gat	att	gca	gtc	ctc	ttc	319
	Val	Ile	Gln	Leu	Val	Leu	Phe	Ile	Ile	Gln	Asp	Ile	Ala	Val	Leu	Phe	
	15				20					25					30		
	aac	atc	atc	atc	att	ttc	ctc	atg	ttc	ttc	aac	acc	tcc	gtc	ttc	cag	367
	Asn	Ile	Ile	Ile	Ile	Phe	Leu	Met	Phe	Phe	Asn	Thr	Ser	Val	Phe	Gln	
				35						40					45		
	gct	ggc	ctg	gtc	aac	ctc	cta	ttc	cat	aag	ttc	aaa	ggg	acc	atc	atc	415
	Ala	Gly	Leu	Val	Asn	Leu	Leu	Phe	His	Lys	Phe	Lys	Gly	Thr	Ile	Ile	
				50				55						60			
	ctg	aca	gct	gtg	tac	ttt	gcc	ctc	agc	atc	tcc	ctt	cat	gtc	tgg	gtc	463
	Leu	Thr	Ala	Val	Tyr	Phe	Ala	Leu	Ser	Ile	Ser	Leu	His	Val	Trp	Val	
			65					70					75				
	atg	aac	tta	cgc	tgg	aaa	aac	tcc	aac	agc	ttc	ata	tgg	aca	gat	gga	511
	Met	Asn	Leu	Arg	Trp	Lys	Asn	Ser	Asn	Ser	Phe	Ile	Trp	Thr	Asp	Gly	
			80				85					90					
	ctt	caa	atg	ctg	ttt	gta	ttc	cag	aga	cta	gca	gca	gtg	ttg	tac	tgc	559
	Leu	Gln	Met	Leu	Phe	Val	Phe	Gln	Arg	Leu	Ala	Ala	Val	Leu	Tyr	Cys	
	95				100						105					110	
	tac	ttc	tat	aaa	cgg	aca	gcc	gta	aga	cta	ggc	gat	cct	cac	ttc	tac	607
	Tyr	Phe	Tyr	Lys	Arg	Thr	Ala	Val	Arg	Leu	Gly	Asp	Pro	His	Phe	Tyr	
				115						120					125		
	cag	gac	tct	ttg	tgg	ctg	cgc	aag	gag	ttc	atg	caa	gtt	cga	agg		652
	Gln	Asp	Ser	Leu	Trp	Leu	Arg	Lys	Glu	Phe	Met	Gln	Val	Arg	Arg		
				130					135				140				
	tgacctcttg	tcacactgat	ggatactttt	ccttctctgat	agaagccaca	tttgctgctt											712
	tgcagggaga	gttggcccta	tgcattgggca	aacagctgga	ctttccaagg	aaggttcaga											772
	ctagcttgt	tcagcattca	agaaggaaga	tccccctct	tgcacaatta	gagtgcccc											832
	atcggtctcc	agtgcggcat	cccttccttg	ccttctacct	ctgttccacc	cccttccttc											892
	ctctctcttc	tgtaccattc	attctccctg	accggccttt	cttgccgagg	gttctgtggc											952
	tcttacccctt	wtgaagcttt	tcttttagcc	tgggacagaa	ggacctccc	gccccaaag											1012
	tgatctcccag	gtgaccaaa	gatgcgaaga	gtgatagtta	cgntgctcct	gactgatcac											1072
	accgcagaca	tttagatttt	tataccaaag	gcactttaaa	aaaatgtttt	ataaatagag											

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<210> 80
<211> 754
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 180..383
<223> Von Heijne matrix
score 4.599999990463257
seq LPFSLVLSMLVTQG/LV
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<221> polyA_signal
<222> 722..727
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<221> polyA site

<222> 743..754

<221> misc_feature

<222> 116..450

<223> homology
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est

<221> misc_feature

<222> 593..710

<223> homology
id :W68799
est

<221> misc_feature

<222> 18..117

<223> homology
id :W68799
est

<221> misc_feature

<222> 561..598

<223> homology
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est

<221> misc_feature

<222> 48..511

<223> homology
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est

<221> misc_feature

<222> 593..673

<223> homology
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est

<221> misc_feature

<222> 535..710

<223> homology
id :W80356
est

<221> misc_feature

<222> 256..405

<223> homology
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est

<221> misc_feature

<222> 432..511

<223> homology
id :W80356
est

<221> misc_feature

<222> 392..437

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<223> homology
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<221> misc_feature
<222> 535..710
<223> homology
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<221> misc_feature
<222> 289..437
<223> homology
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<221> misc_feature
<222> 432..511
<223> homology
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<221> misc_feature
<222> 343..511
<223> homology
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      est

<221> misc_feature
<222> 535..710
<223> homology
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      est

<221> misc_feature
<222> 256..341
<223> homology
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      est

<221> misc_feature
<222> 248..511
<223> homology
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<221> misc_feature
<222> 21..271
<223> homology
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      est

<221> misc_feature
<222> 121..450
<223> homology
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      est

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[illegible][illegible][illegible][illegible][illegible][illegible][illegible]

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<222> 137..291
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<221> misc_feature
<222> 6..91
<223> homology
      id :AA121372
      est

<221> misc_feature
<222> 318..397
<223> homology
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      est

<221> misc_feature
<222> 95..132
<223> homology
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      est

<221> misc_feature
<222> 460..501
<223> homology
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      est

<221> misc_feature
<222> 432..465
<223> homology
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      est

<221> misc_feature
<222> 284..313
<223> homology
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<222> 254..670
<223> homology
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<221> misc_feature
<222> 392..658
<223> homology
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      est

<221> misc_feature
<222> 271..327
<223> homology
      id :T55234

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est

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<223> homology
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<221> misc_feature
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<223> homology
id :AA121362
est

<221> misc_feature
<222> 2..102
<223> homology
id :T53974
est

<221> misc_feature
<222> 150..258
<223> homology
id :T53974
est

<221> misc_feature
<222> 95..171
<223> homology
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est

<221> misc_feature
<222> 322..628
<223> homology
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<221> misc_feature
<222> 445..670
<223> homology
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<221> misc_feature
<222> 2..102
<223> homology
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est

<221> misc_feature
<222> 95..171
<223> homology
id :R09314
est

<221> misc_feature
<222> 150..222

<223> homology
id :R09314
est

<400> 81

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ggcggagaag	ggtgcgggct	cttcgccctt	tgtgtccttc	tttactaac	ttctggactt	120
tccagctctt	ccgaagtctg	ttcttgcgca	aagcccaaag	gctggaaaac	cgtccacg	178
atg acc agc atg act	cag tct ctg cgg	gag gtg ata aag	gcc atg acc			226
Met Thr Ser Met Thr	Gln Ser Leu Arg	Glu Val Ile Lys	Ala Met Thr			
-40	-35	-30	-25			
aag gct cgc aat ttt	gag aga gtt ttg	gga aag att act	ctt gtc tct			274
Lys Ala Arg Asn Phe	Glu Arg Val Leu	Gly Lys Ile Thr	Leu Val Ser			
	-20	-15	-10			
gct gct cct ggg aaa	gtg att tgt gaa	atg aaa gta gaa	gaa gag cat			322
Ala Ala Pro Gly Lys	Val Ile Cys Glu	Met Lys Val Glu	Glu Glu Glu His			
	-5	1	5			
acc aat gca ata ggc	act ctc cac ggc	ggt ttg aca gcc	acg tta gta			370
Thr Asn Ala Ile Gly	Thr Leu His Gly	Gly Gly Leu Thr	Ala Thr Leu Val			
10	15	20				
gat aac ata tca aca	atg gct ctg cta	tgc acg gaa agg	gga gca ccc			418
Asp Asn Ile Ser Thr	Met Ala Leu Leu	Cys Thr Glu Arg	Gly Ala Pro			
25	30	35	40			
gga gtc agt gtc gat	atg aac ata acg	tac atg tca cct	gca aaa tta			466
Gly Val Ser Val Asp	Met Asn Ile Thr	Tyr Met Ser Pro	Ala Lys Leu			
	45	50	55			
gga gag gat ata gtg	att aca gca cat	gtt ctg aag caa	gga aaa aca			514
Gly Glu Asp Ile Val	Ile Thr Ala His	Val Leu Lys Gln	Gly Lys Thr			
	60	65	70			
ctt gca ttt acc tct	gtg ggt ctg acc	aac aag gcc aca	gga aaa tta			562
Leu Ala Phe Thr Ser	Val Gly Leu Thr	Asn Lys Ala Thr	Gly Lys Leu			
	75	80	85			
ata gca caa gga aga	cac aca aaa cac	ctg gga aac tgagagaaca				608
Ile Ala Gln Gly Arg	His Thr Lys His	Leu Gly Asn				
90	95	100				
gcagaatgac ctaaagaaac	ccaacaatga atatcaagta	tagatttgac tcaaacaatt				668
gtaatttttg aaataaacta	gcaaaaccaa aaaaaaaaaa	g				709

<210> 82

<211> 243

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 100..171

<223> Von Heijne matrix

score 3.70000004768372

seq ILFNLLIFLCGFT/NY

<221> polyA_signal

<222> 211..216

<221> polyA_site

<222> 230..243

<221> misc_feature

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<222> 2..164
<223> homology
      id :H64488
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<221> misc_feature
<222> 2..164
<223> homology
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      est

<221> misc_feature
<222> 5..164
<223> homology
      id :AA224847
      est

<221> misc_feature
<222> 10..164
<223> homology
      id :AA161042
      est

<221> misc_feature
<222> 2..84
<223> homology
      id :AA088770
      est

<221> misc_feature
<222> 104..164
<223> homology
      id :AA088770
      est

<221> misc_feature
<222> 10..164
<223> homology
      id :AA100852
      est

<221> misc_feature
<222> 79..164
<223> homology
      id :AA146774
      est

<221> misc_feature
<222> 79..164
<223> homology
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<221> misc_feature
<222> 109..164
<223> homology
      id :AA299239
      est

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<221> misc_feature
<222> 158..207
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<221> misc_feature
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<221> misc_feature
<222> 160..207
<223> homology
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<221> misc_feature
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<221> misc_feature
<222> 160..207
<223> homology
id :AA133048
est

<221> misc_feature
<222> 200..229
<223> homology
id :AA469266
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<221> misc_feature
<222> 200..229
<223> homology
id :AA550735
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<221> misc_feature
<222> 200..229
<223> homology
id :AA601071
est

<221> misc_feature
<222> 200..229
<223> homology

id :AA225190
est

<400> 82

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aactcagtgg caacacccgg gagctgtttt gtcctttgtg gagcctcagc agttccctct 60
ttcagaactc actgccaaga gccctgaaca ggagccacc atg cag tgc ttc agc 114
                                     Met Gln Cys Phe Ser
                                     -20
ttc att aag acc atg atg atc ctc ttc aat ttg ctc atc ttt ctg tgt 162
Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe Leu Cys
      -15      -10      -5
ggc ttc acc aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg 210
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met
      1      5      10
cat aaa cct gtt aca atg taaaaaaaaa aaaaa 243
His Lys Pro Val Thr Met
15
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<210> 83

<211> 829

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 346..408

<223> Von Heijne matrix

score 5.5

seq SFLPSALVIWTS/AF

<221> polyA_signal

<222> 792..797

<221> polyA_site

<222> 817..829

<221> misc_feature

<222> 260..464

<223> homology

id :H57434

est

<221> misc_feature

<222> 118..184

<223> homology

id :H57434

est

<221> misc_feature

<222> 56..113

<223> homology

id :H57434

est

<221> misc_feature

<222> 454..485

<223> homology

id :H57434
est

<221> misc_feature
<222> 118..545
<223> homology
id :N27248
est

<221> misc_feature
<222> 65..369
<223> homology
id :H94779
est

<221> misc_feature
<222> 471..519
<223> homology
id :H94779
est

<221> misc_feature
<222> 61..399
<223> homology
id :H09880
est

<221> misc_feature
<222> 408..452
<223> homology
id :H09880
est

<221> misc_feature
<222> 60..399
<223> homology
id :H29351
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<221> misc_feature
<222> 393..432
<223> homology
id :H29351
est

<221> misc_feature
<222> 260..444
<223> homology
id :AA459511
est

<221> misc_feature
<222> 449..545
<223> homology
id :AA459511
est

<221> misc_feature

	20	25	30	
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtc tta tgt caa				549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln				
	35	40	45	
aaa tagaaatcag gaagataatt caacttaaag aagttcattt catgaccaa				602
Lys				
ctcttcagaa acatgtcttt acaagcatat ctcttgatt gctttctaca ctgttgaatt				662
gtctggcaat atttctgcag tggaaaattt gatttagcta gttcttgact tggataaata				722
tggtaagggtg ggcttttccc cctgtgtaat tggctacsac gtcttacttg agccaagttg				782
gtaagttgaa ataaaatgat watgagagtg acacavaaaa aaaaaaa				829

<210> 84
 <211> 674
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 177..233
 <223> Von Heijne matrix
 score 6.09999990463257
 seq LALLWSLPASDLG/RS

<221> polyA_signal
 <222> 644..649

<221> polyA_site
 <222> 663..674

<221> misc_feature
 <222> 194..592
 <223> homology
 id :AA496246
 est

<221> misc_feature
 <222> 1..100
 <223> homology
 id :AA496246
 est

<221> misc_feature
 <222> 99..202
 <223> homology
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<221> misc_feature
 <222> 187..592
 <223> homology
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<221> misc_feature
 <222> 594..661
 <223> homology
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est

<221> misc_feature
<222> 188..592
<223> homology
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<221> misc_feature
<222> 594..661
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<221> misc_feature
<222> 194..444
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<221> misc_feature
<222> 1..102
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<221> misc_feature
<222> 99..187
<223> homology
id :AA476480
est

<221> misc_feature
<222> 437..592
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est

<221> misc_feature
<222> 594..661
<223> homology
id :AA505488
est

<221> misc_feature
<222> 441..592
<223> homology
id :AA554685
est

<221> misc_feature
<222> 594..661
<223> homology
id :AA554685
est

<221> misc_feature
<222> 414..503

<223> homology
 id :AA215595
 est

<221> misc_feature

<222> 510..539

<223> homology
 id :AA215595
 est

<400> 84

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ataagtgaac cagaccaccc tgatggcatc cacagtgatg tcaaggttgg ggctggccag      60
gggtgggtgg actagaagca tttgggagta gtggccaggg gccctggacg ctagccacgg      120
agctgctgca cagagcctgg tgtccacaag cttccagggtt ggggttggag cctggg atg      179
                                         Met
agc ccc ggc agc gcc ttg gcc ctt ctg tgg tcc ctg cca gcc tct gac      227
Ser Pro Gly Ser Ala Leu Ala Leu Trp Ser Leu Pro Ala Ser Asp
      -15                               -10                               -5
ctg ggc cgg tca gtc att gct gga ctc tgg cca cac act ggc gtt ctc      275
Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val Leu
      1                               5                               10
atc cac ttg gaa aca agc cag tct ttt ctg caa ggt cag ttg acc aag      323
Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr Lys
      15                               20                               25                               30
agc ata ttt ccc ctc tgt tgt aca tcg ttg ttt tgt gtt tgt gtt gta      371
Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val Val
      35                               40                               45
aca gtg ggt gga ggg agg gtg ggg tct aca ttt gtt gca tgagtcgatg      420
Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala
      50                               55
ggtcagaact ttagtatacg catgcgtcct ctgagtgaca gggcattttg tcgaaaataa      480
gcaccttggt aactaaaccc ctctaatagc tataaaggct ttagttctgt attgattaag      540
ttactgtaaa agcttggtt tatttttgta ggacttaatg gctaagaatt agggaacata      600
gcaagggggc tcctctgttg gagtaatgta aattgtaatt ataaataaac atgcaaacct      660
ttaaaaaaaaa aaaa                                                    674

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<210> 85

<211> 478

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 179..319

<223> Von Heijne matrix
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<221> polyA_signal

<222> 461..466

<221> polyA_site

<222> 465..478

<221> misc_feature

<222> 2..464

<223> homology

id :AA310996
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<221> misc_feature
<222> 8..464
<223> homology
id :AA312901
est

<221> misc_feature
<222> 2..416
<223> homology
id :AA401411
est

<221> misc_feature
<222> 2..349
<223> homology
id :R64030
est

<221> misc_feature
<222> 56..464
<223> homology
id :AA400108
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<221> misc_feature
<222> 126..273
<223> homology
id :AA010825
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<221> misc_feature
<222> 2..147
<223> homology
id :AA010825
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<221> misc_feature
<222> 358..435
<223> homology
id :AA010825
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<221> misc_feature
<222> 78..464
<223> homology
id :AA504732
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<221> misc_feature
<222> 90..441
<223> homology
id :H60506
est

<221> misc_feature

<222> 59..349
<223> homology
id :AA346780
est

<221> misc_feature
<222> 2..331
<223> homology
id :AA281167
est

<221> misc_feature
<222> 6..236
<223> homology
id :R35805
est

<221> misc_feature
<222> 232..284
<223> homology
id :R35805
est

<221> misc_feature
<222> 41..307
<223> homology
id :H13784
est

<221> misc_feature
<222> 2..40
<223> homology
id :H13784
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<221> misc_feature
<222> 64..280
<223> homology
id :AA128122
est

<221> misc_feature
<222> 293..349
<223> homology
id :AA128122
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<221> misc_feature
<222> 332..385
<223> homology
id :AA128122
est

<221> misc_feature
<222> 163..420
<223> homology
id :AA555127
est


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<400> 85
aagtccttcg cgccctcctc gccctcccca ccgacatcat gctccagttc ctgcttggat      60
ttacactggg caacgtggtt ggaatgtatc tggctcagaa ctatgatata ccaaacctgg      120
ctaaaaaact tgaagaaatt aaaaaggact tggatgccaa gaagaaaccc cctagtgc      178
atg aga ctg cct cca gca ctg cct tca gga tat act gat tct act gct      226
Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser Thr Ala
      -45                -40                -35
ctt gag ggc ctc gtt tac tat ctg aac caa aag ctt ttg ttt tcg tct      274
Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe Ser Ser
      -30                -25                -20
cca gcc tca gca ctt ctc ttc ttt gct aga ccc tgt gtt ttt tgc ttt      322
Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe Cys Phe
      -15                -10                -5                1
aaa gca agc aaa atg ggg ccc caa ttt gag aac tac cca aca ttt cca      370
Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr Phe Pro
      5                10                15
aca tac tca cct ctt ccc ata atc cct ttc caa ctg cat ggg agg ttc      418
Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly Arg Phe
      20                25                30
taagactgga attatggtgc tagattagta aacatgactt ttaatgaaaa aaaaacaaaa      478

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<210> 86
<211> 952
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 112..237
<223> Von Heijne matrix
      score 7.19999980926514
      seq ILFSLSFLLVIIIT/FP

<221> polyA_signal
<222> 910..915

<221> polyA_site
<222> 940..952

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aatactttct cctctcccct ctcccaagca catctgagtt gctgcctggt cttcacactt      60
agctccaaac ccatgaaaaa ttgccaaagta taaaagcttc tcaagaatga g atg gat      117
                               Met Asp
tct agg gtg tct tca cct gag aag caa gat aaa gag aat ttc gtg ggt      165
Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe Val Gly
      -40                -35                -30                -25
gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg atc ctg ttt tcc ctc      213
Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe Ser Leu
      -20                -15                -10
tct ttc ctg ttg gtg atc att acc ttc ccc atc tcc ata tgg atg tgc      261
Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp Met Cys
      -5                1                5
ttg aag att tgatcctggt cctgccatgc ataratgtgt ttgtcaaagt      310
Leu Lys Ile
      10
tgacctccga acagttactt gcaacattcc tccacaagag atcctcacca rgagactccg      370

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taactactca	ggtagatgga	gttgtctatt	acagaatcta	tagtgctgtc	tcagcagtgg	430
ctaakgtcaa	cgatgtccat	caagcaacat	ttctgctggc	tcaaaccact	ctgagaaatg	490
tcktagggac	acaggacctt	gtccccagat	cttaggctgg	acgagaagag	atcgcccata	550
agcatccaga	ctktacttga	tgatgccacc	gaactggtgg	gggatccggg	tggcccaggt	610
ggaaatcaaa	gatgttcgga	ttcccgtaga	gttgcagaga	tccatggcag	ccgaggstga	670
ggccacccgg	gaagsgagag	ccaaggtcct	tcagactgaa	ggagaaatga	atgsttccaa	730
atccctgaag	tcagcctcca	tggtgstggs	tgagtytccc	atagctytcc	agstgsgsta	790
cctgcagacc	ttgagcacgg	tagccaccga	gaagaatttt	acgattgtgt	ttcctbtgcc	850
catgaatata	ctagagggca	ttggtggcgt	cagstatgat	aaccacaaga	agsttbscaa	910
ataaagcctg	aggtcybctt	gcggtagtca	aaaaaaaaaa	aa		952

<210> 87
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

<400> 87

Met	Leu	Ala	Val	Ser	Leu	Thr	Val	Pro	Leu	Leu	Gly	Ala	Met	Met	Leu	
			-10					-5					1			
Leu	Glu	Ser	Pro	Ile	Asp	Pro	Gln	Pro	Leu	Ser	Phe	Lys	Glu	Pro	Pro	
5						10					15					
Leu	Leu	Leu	Gly	Val	Leu	His	Pro	Asn	Thr	Lys	Leu	Arg	Gln	Ala	Glu	
20					25					30					35	
Arg	Leu	Phe	Glu	Asn	Gln	Leu	Val	Gly	Pro	Glu	Ser	Ile	Ala	His	Ile	
				40				45						50		
Gly	Asp	Val	Met	Phe	Thr	Gly	Thr	Ala	Asp	Gly	Arg	Val	Val	Lys	Leu	
			55					60					65			
Glu	Asn	Gly	Glu	Ile	Glu	Thr	Ile	Ala	Arg	Phe	Gly	Ser	Gly	Pro	Cys	
		70				75					80					
Lys	Thr	Arg	Gly	Asp	Glu	Pro	Val	Cys	Gly	Arg	Pro	Leu	Gly	Ile	Arg	
	85					90				95						
Gly	Arg	Ala	Gln	Trp	Asp	Ser	Leu	Cys	Gly	Arg	Cys	Ile	Gln	Arg	Asp	
100					105					110					115	
Tyr	Leu	Lys														

<210> 88
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35..-1

<400> 88

Met	Leu	Thr	Val	Asn	Asp	Val	Arg	Phe	Tyr	Arg	Asn	Val	Arg	Ser	Asn	
-35					-30					-25					-20	
His	Phe	Pro	Phe	Val	Arg	Leu	Cys	Gly	Leu	Leu	His	Leu	Trp	Leu	Lys	
				-15				-10						-5		
Val	Phe	Ser	Leu	Lys	Gln	Leu	Lys	Lys	Lys	Ser	Trp	Ser	Lys	Tyr	Leu	
		1				5					10					
Phe	Glu	Ser	Cys	Cys	Tyr	Arg	Ser	Leu	Tyr	Val	Cys	Val	Phe	Ile		

15

20

25

<210> 89
 <211> 163
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 89

Met	Ser	Pro	Ala	Phe	Arg	Ala	Met	Asp	Val	Glu	Pro	Arg	Ala	Lys	Gly
-30						-25					-20				
Ser	Phe	Trp	Ser	Pro	Leu	Ser	Thr	Arg	Ser	Gly	Gly	Thr	His	Ala	Cys
-15					-10					-5					1
Ser	Ala	Ser	Met	Arg	Gln	Pro	Trp	Ala	Ser	Pro	Trp	Ser	Gln	Gly	Asn
			5					10					15		
Ile	Ser	Ser	Thr	Arg	Pro	Ser	Leu	Leu	Arg	Cys	Ala	Asn	Ser	Leu	Pro
			20				25					30			
Ser	Thr	Lys	Asp	Lys	Ala	Lys	Gly	Pro	Leu	Leu	Ala	Gly	His	Pro	Cys
			35			40					45				
Pro	Ile	Phe	Ser	Pro	Gly	Pro	Phe	Pro	Cys	Gly	His	Arg	Glu	Val	Trp
50					55					60					65
Pro	Glu	Tyr	Pro	Thr	Pro	Ala	Pro	Leu	His	Pro	Glu	Leu	Gly	Ala	Thr
				70					75					80	
Ser	Glu	Val	Ser	Ser	Leu	Ser	Glu	His	Xaa	Phe	Pro	Cys	Ser	Ser	Arg
			85					90					95		
Gly	Leu	Ser	Arg	Leu	Ser	Asp	Ala	Gly	Ala	Xaa	Xaa	Pro	Glu	Xaa	Lys
			100				105						110		
Gly	Val	Gln	Pro	Val	Val	Cys	Lys	Ala	Leu	Xaa	Gly	Thr	Ala	Glu	Thr
			115			120						125			
Pro	Pro	Pro													
130															

<210> 90
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 90

Met	Leu	Gly	Thr	Thr	Gly	Leu	Gly	Thr	Gln	Gly	Pro	Ser	Gln	Gln	Ala
-30						-25					-20				
Leu	Gly	Phe	Phe	Ser	Phe	Met	Leu	Leu	Gly	Met	Gly	Gly	Cys	Leu	Pro
-15						-10					-5				
Gly	Phe	Leu	Leu	Gln	Pro	Pro	Asn	Arg	Ser	Pro	Thr	Leu	Pro	Ala	Ser
1				5					10					15	
Thr	Phe	Ala	His												
			20												

<210> 91

<211> 124
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -97..-1

<400> 91
 Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val
 -95 -90 -85
 Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val
 -80 -75 -70
 Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly
 -65 -60 -55 -50
 Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys Leu Gly
 -45 -40 -35
 Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr Gln Val
 -30 -25 -20
 Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala Ser Ser
 -15 -10 -5
 Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro
 1 5 10 15
 Leu Phe Glu Glu Leu Arg Gln Val Val Glu Ile Ser
 20 25

<210> 92
 <211> 230
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 92
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
 -20 -15 -10
 Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
 -5 1 5
 Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys
 10 15 20
 Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys
 25 30 35 40
 Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Xaa Ala Ala
 45 50 55
 Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile
 60 65 70
 Ile Ser Val Val Gly Met Xaa Cys Thr Val Phe Cys Gln Glu Ser Arg
 75 80 85
 Ala Lys Asp Arg Val Ala Val Ala Gly Gly Val Phe Phe Ile Leu Gly
 90 95 100
 Gly Leu Leu Gly Phe Ile Pro Val Ala Trp Asn Leu His Gly Ile Leu
 105 110 115 120
 Arg Asp Phe Tyr Ser Pro Leu Val Pro Asp Ser Met Lys Phe Glu Ile
 125 130 135
 Gly Glu Ala Leu Tyr Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile

[illegible]

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<210> 93
<211> 72
<212> PRT
<213> Homo sapiens
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<220>
<221> SIGNAL
<222> -32...-1
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<400> 93															
Met	Phe	Ala	Pro	Ala	Val	Met	Arg	Ala	Phe	Arg	Lys	Asn	Lys	Thr	Leu
		-30					-25					-20			
Gly	Tyr	Gly	Val	Pro	Met	Leu	Leu	Leu	Ile	Val	Gly	Gly	Ser	Phe	Gly
	-15					-10					-5				
Leu	Arg	Glu	Phe	Ser	Gln	Ile	Arg	Tyr	Asp	Ala	Val	Lys	Ser	Lys	Met
1				5					10					15	
Asp	Pro	Glu	Leu	Glu	Lys	Lys	Pro	Lys	Glu	Asn	Lys	Ile	Ser	Leu	Glu
			20					25					30		
Ser	Glu	Tyr	Glu	Gly	Ser	Ile	Cys								
		35					40								

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<210> 94
<211> 91
<212> PRT
<213> Homo sapiens
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<220>  
<221> SIGNAL  
<222> -36..-1
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<400>	94														
Met	Asn	Thr	Phe	Glu	Pro	Asp	Ser	Leu	Ala	Val	Ile	Ala	Phe	Phe	Leu
	-35					-30					-25				
Pro	Ile	Trp	Thr	Phe	Ser	Ala	Leu	Thr	Phe	Leu	Phe	Leu	His	Leu	Pro
-20					-15					-10					-5
Pro	Ser	Thr	Ser	Leu	Phe	Ile	Asn	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Gly
				1				5					10		
Pro	Leu	Gly	Leu	Ile	Leu	Leu	Leu	Ser	Phe	Cys	Gly	Gly	Tyr	Thr	Lys
		15					20					25			
Cys	Asp	Phe	Ala	Leu	Ser	Tyr	Leu	Glu	Ile	Pro	Asn	Arg	Ile	Glu	Phe
	30					35					40				
Ser	Ile	Met	Asp	Pro	Lys	Arg	Lys	Thr	Lys	Cys					
45					50					55					

<210> 95

<211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 95
 Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
 Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
 -15 -10 -5
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Gly Lys Met
 1 5 10 15
 Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
 20 25 30
 Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
 35 40 45
 Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
 50 55 60
 Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
 65 70

<210> 96
 <211> 172
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 96
 Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
 -20 -15 -10
 Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
 -5 1 5 10
 Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
 15 20 25
 Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
 30 35 40
 Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr Lys Gln Val His Ala
 45 50 55
 Leu Ser Pro Glu Glu Asn Val Ile Ile Lys Leu Asn Lys Ala Gly Leu
 60 65 70 75
 Val Leu Gly Ile Leu Ser Cys Leu Gly Leu Ser Ile Val Ala Asn Phe
 80 85 90
 Gln Glu Asn Asn Pro Phe Cys Cys Thr Cys Lys Trp Ser Cys Ala Tyr
 95 100 105
 Leu Trp Tyr Gly Leu Ile Ile Tyr Val Cys Ser Asp His Pro Phe Leu
 110 115 120
 Pro Lys Cys Ser Pro Lys Ser Asn Gly Lys Thr Ser Leu Leu Asp Gln
 125 130 135
 Thr Val Val Gly Tyr Leu Val Trp Ser Lys Cys Thr
 140 145 150

<210> 97
 <211> 56
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

<400> 97
 Met Cys Phe Pro Glu His Arg Arg Gln Met Tyr Ile Gln Asp Arg Leu
 -40 -35 -30
 Asp Ser Val Thr Arg Arg Ala Arg Gln Gly Arg Ile Cys Ala Ile Leu
 -25 -20 -15
 Leu Leu Gln Ser Gln Cys Ala Tyr Trp Ala Leu Pro Glu Pro Arg Thr
 -10 -5 1 5
 Leu Asp Gly Gly His Leu Met Gln
 10

<210> 98
 <211> 46
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 98
 Met Gln Asn His Leu Gln Thr Arg Pro Leu Phe Leu Thr Cys Leu Phe
 -20 -15 -10
 Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu Cys Leu Ile
 -5 1 5 10
 Leu Gln Cys Ser Val Phe Ser Phe Ala Phe Phe Ala Leu Trp
 15 20

<210> 99
 <211> 251
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 99
 Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro
 -25 -20 -15
 Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr
 -10 -5 1
 Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro
 5 10 15 20
 Lys Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys Val Arg Arg
 25 30 35
 Glu Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr

-30 -25 -20
 Ala Leu Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro
 -15 -10 -5 1
 Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser
 5 10 15
 Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser
 20 25 30
 Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp
 35 40 45
 Leu
 50

<210> 102
 <211> 126
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> SIGNAL
 <222> -20..-1

<400> 102
 Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu Leu Thr
 -20 -15 -10 -5
 Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp His Gly
 1 5 10
 Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu Leu Glu Pro
 15 20 25
 Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys Tyr Tyr Ile
 30 35 40
 Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu Ser Phe Phe
 45 50 55 60
 Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu Arg Lys Val
 65 70 75
 Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val Ser His Leu
 80 85 90
 Arg Tyr Phe Gly Ser Ser Arg Gly Lys Ala Phe Ser Leu Thr
 95 100 105

<210> 103
 <211> 273
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> SIGNAL
 <222> -45..-1

<400> 103
 Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
 -45 -40 -35 -30
 Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
 -25 -20 -15
 Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
 -10 -5 1
 Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys

5	10	15													
Phe	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln
20					25					30					35
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala
			40						45					50	
Tyr	Arg	Glu	Val	Gln	Glu	Lys	Arg	His	Arg	Glu	Ala	His	Gly	Glu	Asn
		55					60					65			
Ser	Gly	Arg	Leu	Tyr	Leu	Asn	Pro	Gly	Lys	Lys	Arg	Gly	Gly	Leu	Trp
	70					75					80				
Trp	Thr	Tyr	Val	Cys	Ser	Leu	Val	Phe	Lys	Ala	Ser	Val	Asp	Ile	Ala
	85				90					95					
Phe	Leu	Tyr	Val	Phe	His	Ser	Phe	Tyr	Pro	Lys	Tyr	Ile	Leu	Pro	Pro
100					105					110					115
Val	Val	Lys	Cys	His	Ala	Asp	Pro	Cys	Pro	Asn	Ile	Val	Asp	Cys	Phe
			120						125					130	
Ile	Ser	Lys	Pro	Ser	Glu	Lys	Asn	Ile	Phe	Thr	Leu	Phe	Met	Val	Ala
		135					140						145		
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Val	Glu	Leu	Ile	Tyr	Leu
	150					155					160				
Val	Ser	Lys	Arg	Cys	His	Glu	Cys	Leu	Ala	Ala	Arg	Lys	Ala	Gln	Ala
	165					170					175				
Met	Xaa	Thr	Gly	His	His	Pro	Xaa	Asp	Thr	Thr	Phe	Ser	Xaa	Lys	Gln
180					185					190					195
Xaa	Asp	Xaa	Xaa	Ser	Gly	Asp	Xaa	Ile	Phe	Leu	Gly	Ser	Asp	Ser	His
			200				205							210	
Xaa	Pro	Xaa	Leu	Pro	Asp	Arg	Pro	Arg	Asp	His	Val	Lys	Lys	Thr	Ile
			215				220							225	

Leu

<210> 104
 <211> 158
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 104

Met	Ala	Ser	Lys	Ile	Leu	Leu	Asn	Val	Gln	Glu	Glu	Val	Thr	Cys	Pro
	-35						-30					-25			
Ile	Cys	Leu	Glu	Leu	Leu	Thr	Glu	Pro	Leu	Ser	Leu	Asp	Cys	Gly	His
	-20					-15					-10				
Ser	Leu	Cys	Arg	Ala	Cys	Ile	Thr	Val	Ser	Asn	Lys	Glu	Ala	Val	Thr
-5					1			5						10	
Ser	Met	Gly	Gly	Lys	Ser	Ser	Cys	Pro	Val	Cys	Gly	Ile	Ser	Tyr	Ser
		15					20					25			
Phe	Glu	His	Leu	Gln	Ala	Asn	Gln	His	Arg	Ala	Asn	Ile	Val	Glu	Arg
	30					35					40				
Leu	Lys	Glu	Val	Lys	Leu	Ser	Pro	Asp	Asn	Gly	Lys	Lys	Arg	Asp	Leu
	45				50					55					
Cys	Asp	His	His	Gly	Glu	Lys	Leu	Leu	Leu	Phe	Cys	Lys	Glu	Asp	Arg
60				65					70					75	
Lys	Val	Ile	Cys	Trp	Leu	Cys	Glu	Arg	Ser	Gln	Glu	His	Arg	Gly	His
		80					85					90			
His	Thr	Gly	Pro	His	Gly	Gly	Ser	Ile	Gln	Gly	Met	Ser	Gly	Glu	Thr
		95					100						105		

Pro Gly Ser Pro Gln Glu Ala Glu Glu Gly Arg Gly Gly Ser
 110 115 120

<210> 105
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 105
 Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
 -15 -10 -5
 Val His Thr Thr Leu Ser Lys Ser Asp Ala Xaa Lys Pro Pro Gln Arg
 1 5 10
 Arg Cys Trp Arg Arg Val Ser Phe Gln Ile Ser Arg Cys Lys Thr Gly
 15 20 25
 Val Trp Trp
 30

<210> 106
 <211> 359
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34..-1

<400> 106
 Met Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr
 -30 -25 -20
 Thr Ile Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Leu Leu Pro Val
 -15 -10 -5
 Glu Ala Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe
 1 5 10
 Asp Asp Leu Pro Ala Xaa Phe Gly Tyr Arg Leu Pro Ala Glu Gly Leu
 15 20 25 30
 Lys Gly Phe Leu Ile Asn Ser Lys Pro Glu Asn Ala Cys Glu Pro Ile
 35 40 45
 Val Pro Pro Pro Val Lys Asp Asn Ser Ser Gly Thr Phe Ile Val Leu
 50 55 60
 Ile Xaa Xaa Leu Asp Cys Asn Phe Asp Ile Lys Val Leu Asn Ala Gln
 65 70 75
 Arg Ala Gly Tyr Lys Ala Ala Ile Val His Asn Val Asp Ser Asp Asp
 80 85 90
 Leu Ile Ser Met Gly Ser Asn Asp Ile Glu Val Leu Lys Lys Ile Asp
 95 100 105 110
 Ile Pro Ser Val Phe Ile Gly Glu Ser Ser Ala Ser Ser Leu Lys Asp
 115 120 125
 Glu Phe Thr Xaa Glu Lys Gly Gly His Leu Ile Leu Val Pro Glu Phe
 130 135 140
 Ser Leu Pro Leu Glu Tyr Tyr Leu Ile Pro Phe Leu Ile Xaa Val Gly
 145 150 155

Ile	Cys	Leu	Ile	Leu	Ile	Val	Ile	Phe	Met	Ile	Thr	Lys	Leu	Ser	Arg
160						165					170				
Asp	Arg	His	Arg	Ala	Arg	Arg	Asn	Arg	Leu	Arg	Lys	Asp	Gln	Leu	Lys
175					180					185					190
Lys	Leu	Pro	Val	His	Lys	Phe	Lys	Lys	Gly	Asp	Glu	Tyr	Asp	Val	Cys
				195					200					205	
Ala	Ile	Cys	Leu	Asp	Glu	Tyr	Glu	Asp	Gly	Asp	Lys	Leu	Arg	Ile	Leu
			210					215					220		
Pro	Cys	Ser	His	Ala	Tyr	His	Cys	Lys	Cys	Val	Asp	Pro	Trp	Leu	Thr
		225					230					235			
Lys	Thr	Lys	Lys	Thr	Cys	Pro	Val	Cys	Arg	Gln	Lys	Val	Val	Pro	Ser
	240					245					250				
Gln	Gly	Asp	Ser	Asp	Ser	Asp	Thr	Asp	Ser	Ser	Gln	Glu	Glu	Asn	Glu
255					260					265					270
Val	Thr	Glu	His	Thr	Pro	Leu	Leu	Arg	Pro	Leu	Xaa	Phe	Cys	Gln	Cys
				275					280					285	
Pro	Xaa	Xaa	Phe	Gly	Ala	Leu	Xaa	Gly	Xaa	Pro	Ala	His	Xaa	Gln	Xaa
			290					295					300		
His	Asp	Arg	Ile	Ile	Gln	Thr	Xaa	Glu	Glu	Asp	Asp	Asn	Glu	Asp	Thr
	305					310						315			
Asp	Ser	Ser	Asp	Ala	Glu	Glu									
	320					325									

<210> 107
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

<400> 107

Met	Asp	Ser	Arg	Val	Ser	Ser	Pro	Glu	Lys	Gln	Asp	Lys	Glu	Asn	Phe
	-40						-35					-30			
Val	Gly	Val	Asn	Asn	Lys	Arg	Leu	Gly	Val	Cys	Gly	Trp	Ile	Leu	Phe
	-25					-20					-15				
Ser	Leu	Ser	Phe	Leu	Leu	Val	Ile	Ile	Thr	Phe	Pro	Ile	Ser	Ile	Trp
-10				-5						1				5	
Met	Cys	Leu	Lys	Ile	Ile	Lys	Glu	Tyr	Glu	Arg	Ala	Val	Val	Phe	Arg
		10					15					20			
Leu	Gly	Arg	Ile	Gln	Ala	Asp	Lys	Ala	Lys	Gly	Pro	Gly	Leu	Ile	Leu
	25					30						35			
Val	Leu	Pro	Cys	Ile	Asp	Val	Phe	Val	Lys	Val	Asp	Leu	Arg	Thr	Val
	40					45					50				
Thr	Cys	Asn	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Arg	Asp	Ser	Val	Thr
55				60						65					70
Thr	Gln	Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Ile	Tyr	Ser	Ala	Val	Ser
				75					80					85	
Ala	Val	Ala	Asn	Val	Asn	Asp	Val	His	Gln	Ala	Thr	Phe	Leu	Leu	Ala
			90					95					100		
Gln	Thr	Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Gln	Thr	Leu	Ser	Gln	Ile
	105						110					115			
Leu	Ala	Gly	Arg	Glu	Glu	Ile	Ala	His	Ser	Ile	Gln	Thr	Leu	Leu	Asp
	120					125					130				
Asp	Ala	Thr	Glu	Leu	Trp	Gly	Ile	Arg	Val	Ala	Arg	Val	Glu	Ile	Lys
135					140					145					150

Asp Val Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala
 155 160 165
 Glu Ala Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu
 170 175 180
 Met Ser Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu
 185 190 195
 Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val
 200 205 210
 Ala Thr Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile
 215 220 225 230
 Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro
 235 240 245
 Asn Lys Ala

<210> 108
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 108
 Met Ser Thr Trp Leu Leu Leu Ile Ala Leu Lys Thr Leu Ile Thr Trp
 -25 -20 -15
 Val Ser Leu Phe Ile Asp Cys Val Met Thr Arg Lys Leu Thr Asn Cys
 -10 -5 1 5
 Asn Ala Arg Glu Thr Ile Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn
 10 15 20
 Cys Phe Ala Ile Arg His Phe Glu Asn Lys Phe Ala Val Glu Thr Leu
 25 30 35
 Ile Cys Ser
 40

<210> 109
 <211> 127
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -63..-1

<400> 109
 Met Ser Ala Ala Gly Ala Arg Gly Leu Arg Ala Thr Tyr His Arg Leu
 -60 -55 -50
 Leu Asp Lys Val Glu Leu Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr
 -45 -40 -35
 Asn His Pro Ala Gly Pro Arg Thr Val Phe Phe Trp Ala Pro Ile Met
 -30 -25 -20
 Lys Trp Gly Leu Val Cys Ala Gly Leu Ala Asp Met Ala Arg Pro Ala
 -15 -10 -5 1
 Glu Lys Leu Ser Thr Ala Gln Ser Ala Val Leu Met Ala Thr Gly Phe
 5 10 15
 Ile Trp Ser Arg Tyr Ser Leu Val Ile Ile Pro Lys Asn Trp Ser Leu

	20					25				30					
Phe	Ala	Val	Asn	Phe	Phe	Val	Gly	Ala	Ala	Gly	Ala	Ser	Gln	Leu	Phe
	35					40				45					
Arg	Ile	Trp	Arg	Tyr	Asn	Gln	Glu	Leu	Lys	Ala	Lys	Ala	His	Lys	
50					55					60					

<210> 110
 <211> 97
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 110
 Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
 -20 -15 -10 -5
 Thr Ala Trp Ala Arg Arg Ser Arg Asp Leu His Cys Gly Ala Cys Arg
 1 5 10
 Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
 15 20 25
 Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln
 30 35 40
 Ser Val Val Glu Val Thr Val Thr Xaa Ser Pro Lys Thr Lys Val Ala
 45 50 55 60
 His Ser Gly Phe Trp Met Lys Ile Arg Leu Lys Lys Gly Pro Trp
 65 70 75
 Ser

<210> 111
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 111
 Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
 -20 -15 -10 -5
 Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg
 1 5 10
 Ala Leu Val Asp Glu Thr Arg Met Gly Asn Cys Pro Gly Gly Pro Gln
 15 20 25
 Glu Asp His Ser Asp Gly Ile Phe Pro Asp Gln Ser Arg Trp Gln Pro
 30 35 40
 Val Ser Gly Gly Gly Ala Leu Cys Pro Leu Arg Gly Pro Pro His Arg
 45 50 55 60
 Ala Ala Gly Gly Asp Met
 65

<210> 112
 <211> 71

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 112

Met	Pro	Ala	Gly	Val	Pro	Met	Ser	Thr	Tyr	Leu	Lys	Met	Phe	Ala	Ala	
-25					-20					-15						-10
Ser	Leu	Leu	Ala	Met	Cys	Ala	Gly	Ala	Glu	Val	Val	His	Arg	Tyr	Tyr	
			-5					1				5				
Arg	Pro	Asp	Leu	Thr	Ile	Pro	Glu	Ile	Pro	Pro	Lys	Arg	Gly	Glu	Leu	
	10						15					20				
Lys	Thr	Glu	Leu	Leu	Gly	Leu	Lys	Glu	Arg	Lys	His	Lys	Pro	Gln	Val	
25						30					35					
Ser	Gln	Gln	Glu	Glu	Leu	Lys										
40					45											

<210> 113
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 113

Met	Asp	Gly	His	Trp	Ser	Ala	Ala	Phe	Ser	Ala	Leu	Thr	Val	Thr	Ala	
	-40						-35					-30				
Met	Ser	Ser	Trp	Ala	Arg	Arg	Arg	Ser	Ser	Ser	Ser	Arg	Arg	Ile	Pro	
	-25				-20						-15					
Ser	Leu	Pro	Gly	Ser	Pro	Val	Cys	Trp	Ala	Trp	Pro	Trp	Tyr	Pro	Asp	
-10					-5				1					5		
Thr	Thr	Ser	Phe	Pro	Leu	Arg	Cys	Arg	Gly	Arg	Val					
			10					15								

<210> 114
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -83..-1

<400> 114

Met	Leu	Pro	Val	Gln	Ser	Phe	Thr	Leu	Val	Ala	Gln	Ala	Gly	Val	Gln	
			-80					-75					-70			
Trp	Arg	His	Leu	Ser	Ser	Leu	Gln	Leu	Leu	Pro	Pro	Glu	Phe	Lys	Gly	
		-65					-60					-55				
Phe	Ser	Cys	Leu	Ser	Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Arg	Arg	Pro	Pro	
	-50					-45					-40					
Pro	Cys	Pro	Ala	Gly	Phe	Phe	Val	Phe	Leu	Val	Glu	Thr	Gly	Leu	His	
-35					-30					-25					-20	

His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Cys Ser Pro Pro
 -15 -10 -5
 Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val Ser His Val Pro
 1 5 10
 Gly Lys Lys Lys Leu Leu Lys Val Glu Lys Lys Asn Leu Arg Xaa Leu
 15 20 25
 Leu Thr Xaa Ile Lys Thr
 30 35

<210> 115
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 115
 Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
 -20 -15 -10
 Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
 -5 1 5 10
 Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Xaa Phe Gly Lys Ala
 15 20 25
 Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Val Cys Gly Arg Gly
 30 35 40
 Xaa Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu Phe
 45 50

<210> 116
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -52...-1

<400> 116
 Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys Asp
 -50 -45 -40
 Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala
 -35 -30 -25
 Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu Leu
 -20 -15 -10 -5
 Val Ser Leu Gly Gln Ser Ile Trp Leu His Ile Thr Glu Asn Gln Ile
 1 5 10
 Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu Lys
 15 20 25
 Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln
 30 35 40

<210> 117
 <211> 82
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -22..-1

<400> 117

Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
-20 -15 -10
Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
-5 1 5 10
Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala
15 20 25
Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Tyr Gly Pro Ile Phe
30 35 40
Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe Val Thr Glu Glu Gly
45 50 55
Arg Asn
60

<210> 118

<211> 89

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 118

Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
-15 -10 -5
Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
1 5 10 15
Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
20 25 30
Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile
35 40 45
Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp Trp Ala
50 55 60
Glu Ala Gly Ala Ser Leu Tyr Ser Pro
65 70

<210> 119

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19..-1

<400> 119

Met Thr Met Ala Glu Cys Pro Thr Leu Cys Val Ser Ser Ser Pro Ala
-15 -10 -5
Leu Trp Ala Ala Ser Glu Thr Thr Asp Asp Val Cys Arg Glu

<210> 120
 <211> 115
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -103...-1

<400> 120
 Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile
 -100 -95 -90
 Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile
 -85 -80 -75
 Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp
 -70 -65 -60
 Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala Thr Gly Asn Pro
 -55 -50 -45 -40
 Leu Pro Pro Gln Ile Phe Asn Glu Ser Gln Tyr Arg Gly Asp Tyr Asp
 -35 -30 -25
 Ala Phe Phe Glu Ala Arg Glu Asn Asn Ala Val Tyr Ala Phe Leu Gly
 -20 -15 -10
 Leu Thr Ala Pro Ser Gly Ser Lys Glu Ala Gly Arg Cys Lys Gln Ser
 -5 1 5
 Ser Lys Pro
 10

<210> 121
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -76...-1

<400> 121
 Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr Leu Leu Leu Lys Trp
 -75 -70 -65
 Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp Leu Val Ser Tyr Pro
 -60 -55 -50 -45
 Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn Leu Asp Phe Pro Lys
 -40 -35 -30
 Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr Arg Trp Phe Asn Leu
 -25 -20 -15
 Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala Ser Ser Ser Ala Asn
 -10 -5 1
 Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro Leu Phe Glu
 5 10 15 20
 Glu Leu Arg Gln Val Val Glu Val Ser
 25

<210> 122

<211> 93
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 122
 Met Lys Pro Val Leu Pro Leu Gln Phe Leu Val Val Phe Cys Leu Ala
 -20 -15 -10
 Leu Gln Leu Val Pro Gly Ser Pro Lys Gln Arg Val Leu Lys Tyr Ile
 -5 1 5 10
 Leu Glu Pro Pro Pro Cys Ile Ser Ala Pro Glu Asn Cys Thr His Leu
 15 20 25
 Cys Thr Met Gln Glu Asp Cys Glu Lys Gly Phe Gln Cys Cys Ser Ser
 30 35 40
 Phe Cys Gly Ile Val Cys Ser Ser Glu Thr Phe Gln Lys Arg Asn Arg
 45 50 55
 Ile Lys His Lys Gly Ser Glu Val Ile Met Pro Ala Asn
 60 65 70

<210> 123
 <211> 109
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

<400> 123
 Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala
 -40 -35 -30
 Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe
 -25 -20 -15
 Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Ala Ile Ile
 -10 -5 1 5
 Leu Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser
 10 15 20
 Ala Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys
 25 30 35
 Val Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met
 40 45 50
 Glu Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Gly Val
 55 60 65

<210> 124
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 124

Met Arg Leu Val Pro Leu Gly Gln Ser Phe Pro Leu Ser Glu Pro Arg
-15 -10 -5 1
Cys Leu Gln Pro Val Lys Trp Asp His Asn His Cys Leu Thr Ser Leu
5 10 15
Thr Val Val Val Arg Thr Glu Cys Val Glu Val Phe His Lys Leu Trp
20 25 30
Met Leu Val
35

<210> 125

<211> 56

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27..-1

<400> 125

Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile Cys Leu
-25 -20 -15
Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg
-10 -5 1 5
Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val Arg Ala
10 15 20
Trp Cys Ile Gln Pro Trp Ala Lys
25

<210> 126

<211> 162

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21..-1

<400> 126

Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
-20 -15 -10
Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
-5 1 5 10
Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala
15 20 25
Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Ser
30 35 40
Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly
45 50 55
Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His
60 65 70 75
Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp
80 85 90
Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val
95 100 105
Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro

110	115	120
His Phe Tyr Gln Asp Ser	Leu Trp Leu Arg Lys	Glu Phe Met Gln Val
125	130	135
Arg Arg		
140		

<210> 127
 <211> 126
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -68..-1

<400> 127
 Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
 -65 -60 -55
 Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
 -50 -45 -40
 His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
 -35 -30 -25
 Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
 -20 -15 -10 -5
 Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
 1 5 10
 Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
 15 20 25
 Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
 30 35 40
 Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Thr Ala
 45 50 55

<210> 128
 <211> 140
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40..-1

<400> 128
 Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr
 -40 -35 -30 -25
 Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser
 -20 -15 -10
 Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu Glu His
 -5 1 5
 Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val
 10 15 20
 Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro
 25 30 35 40
 Gly Val Ser Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu
 45 50 55
 Gly Glu Asp Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr

		60						65						70					
Leu	Ala	Phe	Thr	Ser	Val	Gly	Leu	Thr	Asn	Lys	Ala	Thr	Gly	Lys	Leu				
		75					80					85							
Ile	Ala	Gln	Gly	Arg	His	Thr	Lys	His	Leu	Gly	Asn								
	90					95					100								

<210> 129
 <211> 43
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 129
 Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 -20 -15 -10
 Leu Ile Phe Leu Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser
 -5 1 5
 Pro Tyr Phe Lys Met His Lys Pro Val Thr Met
 10 15

<210> 130
 <211> 69
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 130
 Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
 -20 -15 -10
 Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
 -5 1 5 10
 Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
 15 20 25
 Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
 30 35 40
 Val Leu Cys Gln Lys
 45

<210> 131
 <211> 78
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 131
 Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser

				-15					-10					-5			
Asp	Leu	Gly	Arg	Ser	Val	Ile	Ala	Gly	Leu	Trp	Pro	His	Thr	Gly	Val		
			1				5					10					
Leu	Ile	His	Leu	Glu	Thr	Ser	Gln	Ser	Phe	Leu	Gln	Gly	Gln	Leu	Thr		
	15					20					25						
Lys	Ser	Ile	Phe	Pro	Leu	Cys	Cys	Thr	Ser	Leu	Phe	Cys	Val	Cys	Val		
30					35					40					45		
Val	Thr	Val	Gly	Gly	Gly	Arg	Val	Gly	Ser	Thr	Phe	Val	Ala				
				50					55								

<210> 132
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47..-1

Met	Arg	Leu	Pro	Pro	Ala	Leu	Pro	Ser	Gly	Tyr	Thr	Asp	Ser	Thr	Ala		
			-45				-40					-35					
Leu	Glu	Gly	Leu	Val	Tyr	Tyr	Leu	Asn	Gln	Lys	Leu	Leu	Phe	Ser	Ser		
	-30					-25					-20						
Pro	Ala	Ser	Ala	Leu	Leu	Phe	Phe	Ala	Arg	Pro	Cys	Val	Phe	Cys	Phe		
-15					-10				-5						1		
Lys	Ala	Ser	Lys	Met	Gly	Pro	Gln	Phe	Glu	Asn	Tyr	Pro	Thr	Phe	Pro		
			5				10						15				
Thr	Tyr	Ser	Pro	Leu	Pro	Ile	Ile	Pro	Phe	Gln	Leu	His	Gly	Arg	Phe		
		20					25					30					

<210> 133
 <211> 53
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

Met	Asp	Ser	Arg	Val	Ser	Ser	Pro	Glu	Lys	Gln	Asp	Lys	Glu	Asn	Phe		
	-40						-35					-30					
Val	Gly	Val	Asn	Asn	Lys	Arg	Leu	Gly	Val	Cys	Gly	Trp	Ile	Leu	Phe		
	-25					-20					-15						
Ser	Leu	Ser	Phe	Leu	Leu	Val	Ile	Ile	Thr	Phe	Pro	Ile	Ser	Ile	Trp		
-10					-5				1					5			
Met	Cys	Leu	Lys	Ile													
				10													

<210> 134
 <211> 1053
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 131..169
 <223> Von Heijne matrix
 score 4.19999980926514
 seq MLAVSLTVPLLGA/MM

<221> polyA_site
 <222> 1042..1053

<400> 134

gagcagagtcg gacgggctgc gacagcgccg gcccctgcgg ccgcaggtcg tcacagacga	60
tgatggccag gccccggagg ctaaggacgg cagctccttt agcggcagag ttttccgagt	120
gaccttcttg atg ctg gct gtt tct ctc acc gtt ccc ctg ctt gga gcc	169
Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala	
-10 -5	
atg atg ctg ctg gaa tct cct ata gat cca cag cct ctc agc ttc aaa	217
Met Met Leu Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys	
1 5 10 15	
gaa ccc ccg ctc ttg ctt ggt gtt ctg cat cca aat acg aag ctg cga	265
Glu Pro Pro Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg	
20 25 30	
cag gca gaa agg ctg ttt gaa aat caa ctt gtt gga ccg gag tcc ata	313
Gln Ala Glu Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile	
35 40 45	
gca cat att ggg gat gtg atg ttt act ggg aca gca gat ggc cgg gtc	361
Ala His Ile Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val	
50 55 60	
gta aaa ctt gaa aat ggt gaa ata gag acc att gcc cgg ttt ggt tcg	409
Val Lys Leu Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser	
65 70 75 80	
ggc cct tgc aaa acc cga ggt gat gag cct gtg tgt ggg aga ccc ctg	457
Gly Pro Cys Lys Thr Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu	
85 90 95	
ggg atc cgt gca ggg ccc aat ggg act ctc ttt gtg gcc gat gca tac	505
Gly Ile Arg Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Tyr	
100 105 110	
aag gga cta ttt gaa gta aat ccc tgg aaa cgt gaa gtg aaa ctg ctg	553
Lys Gly Leu Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu	
115 120 125	
ctg tcc tcc gag aca ccc att gag ggg aag aac atg tcc ttt gtg aat	601
Leu Ser Ser Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn	
130 135 140	
gat ctt aca gtc act cag gat ggg agg aag att tat ttc acc gat tct	649
Asp Leu Thr Val Thr Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser	
145 150 155 160	
agc agc aaa tgg caa aga cga gac tac ctg ctt ctg gtg atg gag ggc	697
Ser Ser Lys Trp Gln Arg Arg Asp Tyr Leu Leu Leu Val Met Glu Gly	
165 170 175	
aca gat gac ggg cgc ctg ctg gag tat gat act gtg acc agg gaa gta	745
Thr Asp Asp Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val	
180 185 190	
aaa gtt tta ttg gac cag ctg cgg ttc ccg aat gga gtc cag ctg tct	793
Lys Val Leu Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser	
195 200 205	
cct gca gaa gac ttt gtc ctg gtg gca gaa aca acc atg gcc agg ata	841
Pro Ala Glu Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile	
210 215 220	

cga aga gtc tac gtt tct ggc ctg atg aag ggc ggg gct gat ctg ttt	889
Arg Arg Val Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe	
225 230 235 240	
gtg gag aac atg cct gga ttt cca gac aac atc cgg ccc agc agc tct	937
Val Glu Asn Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser	
245 250 255	
ggg ggg tac tgg gtg ggc atg tcg acc atc cgc cct aac cct ggg ttt	985
Gly Gly Tyr Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe	
260 265 270	
tcc atg ctg gat ttc tta tct gag aga ccc tgg att aaa agg atg att	1033
Ser Met Leu Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile	
275 280 285	
ttt aag gta aaaaaaaaaa a	1053
Phe Lys Val	
290	

<210> 135
 <211> 675
 <212> DNA
 <213> Homo sapiens

<220>
 <221> polyA_signal
 <222> 638..643

<221> polyA_site
 <222> 662..675

<400> 135
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 gtagcagtgg ttcagcacac tttggtatgt tgactgtta atg atg tac gtt tct 114
 Met Met Tyr Val Ser
 1 5
 ata gaa atg tca ggt cca acc att tcc cat ttg ttc gac tat gtg gtc 162
 Ile Glu Met Ser Gly Pro Thr Ile Ser His Leu Phe Asp Tyr Val Val
 10 15 20
 tgt tac att tat ggc tta aag tcc ttt tct ctt aaa cag tta aaa aaa 210
 Cys Tyr Ile Tyr Gly Leu Lys Ser Phe Ser Leu Lys Gln Leu Lys Lys
 25 30 35
 aaa tct tgg tct aag tat tta ttt gaa tcc tgt tgc tat agg agt ttg 258
 Lys Ser Trp Ser Lys Tyr Leu Phe Glu Ser Cys Cys Tyr Arg Ser Leu
 40 45 50
 tat gtg tgt gtc ttc att taaacatacc tgcatacaaa gatggtttat 306
 Tyr Val Cys Val Phe Ile
 55
 ttctatttaa tatgtgacat ttgtttcctg gatatagtcc gtgaaccaca agatttatca 366
 tatttttcaa taatatgaga agaaaatggg ccgtaaattg ttaaccattt tatgttcaga 426
 tattttctcta gtttttacct agtttgcttt aacatagaga ccagcaagtg aatatatatg 486
 cataacctta tatgttgaca caataattca gaataatttg ttaaagataa actaattttt 546
 cagagaagaa catttaagg gttaatatatt ttgaaacggt ttcagataat atctatttga 606
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 aaaaaaaaaa 675

<210> 136
 <211> 1112
 <212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 111..194

<223> Von Heijne matrix

score 4.80000019073486

seq GVLLEPFVHQVGG/HS

<221> polyA_signal

<222> 1080..1085

<221> polyA_site

<222> 1101..1112

<400> 136

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ccgctggact ccgctgcctc ccccatctcc ccgccatctg cgcccggagg atg agc 116

Met Ser

cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc gtc ctt 164

Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu

-25 -20 -15

ctg gag ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc 212

Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg

-10 -5 1 5

ttc aat gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag 260

Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln

10 15 20

ttc tac gag acc ctc cct gct gag atg cgc aaa ttc tct ccc cag tac 308

Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Ser Pro Gln Tyr

25 30 35

aaa gga caa agc caa agg ccc ctt gtt agc tgg cca tcc ctg ccc cat 356

Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp Pro Ser Leu Pro His

40 45 50

ttt ttc ccc tgg tcc ttt ccc ctg tgg cca cag gga agt gtg gcc 401

Phe Phe Pro Trp Ser Phe Pro Leu Trp Pro Gln Gly Ser Val Ala

55 60 65

tgaatacccc accccggctc ctctgcaccc agagctgggg gccacctcag aagtgtcatc 461

tctctctgag cacgcattcc cctgcagcag tcgaggactg agcagattga gtgatgctgg 521

ggcagagagg cctgagagga aaggtgttca gccagtcgtt tgtaaggcgc tcgtcggcac 581

ctgctgaaac gccccacct gacagcccca tcctcaaaga ctgtcttaat tactcatggc 641

aggttctaga gacttaaggg gaaaagctgc tttcaaggcc accacatgtc tgtgctcccc 701

aaccagctct atctgccttg tgttcatttt gttattttgt gacgtgagac agcaaagacc 761

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gctttgctta cccagtcttc ccttactctt ggatgcttct taaccctcag gcaaacctgt 941

gttccccctg tattcaggct ctgctttaaa gcaagccatg aggctgttgg agtttctgtt 1001

tagggcatta aaaattccc caaactataa agagcaatgt tttcagtctt ttaggattag 1061

aagaattaca taaaaattaa taaacatttt caatgatgga aaaaaaaaaa a 1112

<210> 137

<211> 547

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 359..454
 <223> Von Heijne matrix
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<221> polyA_site
 <222> 536..547

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 gggttttattg tgagctggcc ttggaattaa accaccacca acacactttt ggattatcag 180
 aagggtggaag gagtgcaaaa atgtcattcc catgcttgct tgccaggcaa cctgggtgtcc 240
 attctttatg acgcctttcc tgaatcacag gtgcattggg gtgcttcctc ctcccagga 300
 ctcccaccca actttgtgaa cacaaccac ttagaggagt tatctcagca cattatga 358
 atg ttg ggg acc acg ggc ctc ggg aca cag ggt cct tcc cag cag gct 406
 Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala
 -30 -25 -20
 ctg ggc ttt ttc tcc ttt atg tta ctt gga atg ggc ggc tgc ctg cct 454
 Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro
 -15 -10 -5
 gga ttc ctg cta cag cct ccc aat cga tct cct act ttg cct gca tcc 502
 Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser
 1 5 10 15
 acc ttt gcc cat taaagtcaat tctccaccca taaaaaaaaa aaa 547
 Thr Phe Ala His
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<210> 138
 <211> 1198
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 26..316
 <223> Von Heijne matrix
 score 4
 seq RLPLVVVSFIASSS/AN

<221> polyA_signal
 <222> 1164..1169

<221> polyA_site
 <222> 1187..1198

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 Met Ala Asp Asp Leu Lys Arg Phe Leu
 -95 -90
 tat aaa aag tta cca agt gtt gaa ggg ctc cat gcc att gtt gtg tca 100
 Tyr Lys Lys Leu Pro Ser Val Glu Gly Leu His Ala Ile Val Val Ser
 -85 -80 -75
 gat aga gat gga gta cct gtt gtt aaa gtg gca aat gac aat gct cca 148
 Asp Arg Asp Gly Val Pro Val Val Lys Val Ala Asn Asp Asn Ala Pro
 -70 -65 -60
 gag cat gct ttg cga cct ggt ttc tta tcc act ttt gcc ctt gca aca 196

Glu His Ala Leu Arg Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr	
-55 -50 -45	
gac caa gga agc aaa ctt gga ctt tcc aaa aat aaa agt atc atc tgt	244
Asp Gln Gly Ser Lys Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys	
-40 -35 -30 -25	
tac tat aac acc tac cag gtg gtt caa ttt aat cgt tta cct ttg gtg	292
Tyr Tyr Asn Thr Tyr Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val	
-20 -15 -10	
gtg agt ttc ata gcc agc agc agt gcc aat aca gga cta att gtc agc	340
Val Ser Phe Ile Ala Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser	
-5 1 5	
cta gaa aag gag ctt gct cca ttg ttt gaa gaa ctg aga caa gtt gtg	388
Leu Glu Lys Glu Leu Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val	
10 15 20	
gaa gtt tct taatctgaca gtgggttcag tgtgtacctt atcttcatta	437
Glu Val Ser	
25	
taacaacaca atatcaatcc agcaatcttt agactacaat aatgcttttta tccatgtgct	497
caagaaaggg cccctttttc caacttatac taaagagcta gcatatagat gtaatttata	557
gatagatcag ttgctatatatt ttctgggtgta gggtctttct tatttagtga gatctaggga	617
taccacagaa atgggttcagt ctatcacagc tcccatggag ttagtctgggt caccagatat	677
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acatatattt ttgcagtata gatgaatatt actaatcagt ttgattattc tcagagggtg	977
ctgctcttta atgaaaatga aaattatagc taatgttttt tcctcaaact ctgctttctg	1037
taaccaatca gtgttttaaat gtttgtgtgt tcttcataaa atttaaatac aattcgttat	1097
tctgtttcca atgttagtat gtatgtaaac atgatagtac agccattttt ttcatatgtg	1157
agtaaaaata aaatagtatt tttaaaagta aaaaaaaaaa a	1198

<210>	139
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<212>	DNA
<213>	Homo sapiens
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<221>	polyA_signal
<222>	1302..1307
<221>	polyA_site
<222>	1389..1400
<400>	139
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	Met Ala Ser Leu Gly Leu
	-20
caa ctt gtg ggc tac atc cta ggc ctt ctg ggg ctt ttg ggc aca ctg	101
Gln Leu Val Gly Tyr Ile Leu Gly Leu Gly Leu Leu Gly Thr Leu	
-15 -10 -5	
gtt gcc atg ctg ctc ccc agc tgg aaa aca agt tct tat gtc ggt gcc	149

Val	Ala	Met	Leu	Leu	Pro	Ser	Trp	Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala		
		1				5					10						
agc	att	gtg	aca	gca	gtt	ggc	ttc	tcc	aag	ggc	ctc	tgg	atg	gaa	tgt	197	
Ser	Ile	Val	Thr	Ala	Val	Gly	Phe	Ser	Lys	Gly	Leu	Trp	Met	Glu	Cys		
15					20					25					30		
gcc	aca	cac	agc	aca	ggc	atc	acc	cag	tgt	gac	atc	tat	agc	acc	ctt	245	
Ala	Thr	His	Ser	Thr	Gly	Ile	Thr	Gln	Cys	Asp	Ile	Tyr	Ser	Thr	Leu		
				35					40					45			
ctg	ggc	ctg	ccc	gct	gac	atc	cag	gct	gcc	cag	gcc	atg	atg	gtg	aca	293	
Leu	Gly	Leu	Pro	Ala	Asp	Ile	Gln	Ala	Ala	Gln	Ala	Met	Met	Val	Thr		
			50					55				60					
tcc	agt	gca	atc	tcc	tcc	ctg	gcc	tgc	att	atc	tct	gtg	gtg	ggc	atg	341	
Ser	Ser	Ala	Ile	Ser	Ser	Leu	Ala	Cys	Ile	Ile	Ser	Val	Val	Gly	Met		
		65				70					75						
aga	tgc	aca	gtc	ttc	tgc	cag	gaa	tcc	cga	gcc	aaa	gac	aga	gtg	gcg	389	
Arg	Cys	Thr	Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala		
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gta	gca	ggg	gga	gtc	ttt	ttc	atc	ctt	gga	ggc	ctc	ctg	gga	ttc	att	437	
Val	Ala	Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile		
		95			100				105					110			
cct	gtt	gcc	tgg	aat	ctt	cat	ggg	atc	cta	cgg	gac	ttc	tac	tca	cca	485	
Pro	Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro		
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ctg	gtg	cct	gac	agc	atg	aaa	ttt	gag	att	gga	gag	gct	ctt	tac	ttg	533	
Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr	Leu		
			130					135				140					
ggc	att	att	tct	tcc	ctg	ttc	tcc	ctg	ata	gct	gga	atc	atc	ctc	tgc	581	
Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile	Leu	Cys		
		145				150					155						
ttt	tcc	tgc	tca	tcc	cag	aga	aat	cgc	tcc	aac	tac	tac	gat	gcc	tac	629	
Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr	Asp	Ala	Tyr		
		160				165					170						
caa	gcc	caa	cct	ctt	gcc	aca	agg	agc	tct	cca	agg	cct	ggg	caa	cct	677	
Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg	Pro	Gly	Gln	Pro		
		175			180					185				190			
ccc	aaa	gtc	aag	agt	gag	ttc	aat	tcc	tac	agc	ctg	aca	ggg	tat	gtg	725	
Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr	Ser	Leu	Thr	Gly	Tyr	Val		
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<210> 140
 <211> 538
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 <213> Homo sapiens

<220>

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<222> 35..130
<223> Von Heijne matrix
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<222> 505..510

<221> polyA_site
<222> 526..538

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                               -30
cgt gct ttt cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg      103
Arg Ala Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu
-25                -20                -15                -10
ttg ctg att gct gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc      151
Leu Leu Ile Ala Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile
                -5                1                5
cga tat gat gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa      199
Arg Tyr Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys
                10                15                20
ccg aaa gag aat aaa ata tct tta gag tcg gaa tat gag gga agt atc      247
Pro Lys Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Gly Ser Ile
                25                30                35
tgt tgaagggcta ctatctttcc ttggcccttc tcccttggtg ggactcaatc      300
Cys
40
tccagactat ctccccagag aatcttgtca aggcttggct ttaagctttg ttgggaaaat      360
caaagactcc aagtttgatg actggaagaa tattcgagga ccaggcctt gggaagatcc      420
tgacctcctc caaggaagaa atccagaaaag ccttaagact aagacaactt gactctgctg      480
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<210> 141
<211> 1167
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 169..267
<223> Von Heijne matrix
      score 7.80000019073486
      seq LTFLFLHLPPSTS/LF

<221> polyA_signal
<222> 1132..1137

<221> polyA_site
<222> 1155..1167

<400> 141
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cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg att	220
Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile	
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gtt gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc cga tat gat	268
Val Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp	
-5 1 5 10	
gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa gag	316
Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu	
15 20 25	
aat aaa ata tct tta gag tcg gaa tat gag aaa atc aaa gac tcc aag	364
Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys	
30 35 40	
ttt gat gac tgg aag aat att cga gga ccc agg cct tgg gaa gat cct	412
Phe Asp Asp Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro	
45 50 55	
gac ctc ctc caa gga aga aat cca gaa agc ctt aag act aag aca act	460
Asp Leu Leu Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr	
60 65 70	
tgactctgct gattctcttt tccttttttt ttttaaataa aaatactatt aactggactt	520
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<210> 143
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 <213> Homo sapiens

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 <222> 108..170
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<221> polyA_signal
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<221> polyA_site
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Met Trp Trp	
-20	
ttt cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca	164
Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr	
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tct gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat	212
Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His	
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ata gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca	260
Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro	
15 20 25 30	
gaa aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgc	308

Glu	Lys	Cys	Leu	Phe	Gly	Ala	Met	Leu	Asn	Ile	Ala	Ala	Val	Leu	Cys		
			35					40					45				
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Ile	Ala	Thr	Ile	Tyr	Val	Arg	Tyr	Lys	Gln	Val	His	Ala	Leu	Ser	Pro		
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Glu	Glu	Asn	Val	Ile	Ile	Lys	Leu	Asn	Lys	Ala	Gly	Leu	Val	Leu	Gly		
		65					70					75					
ata	ctg	agt	tgt	tta	gga	ctt	tct	att	gtg	gca	aac	ttc	cag	aaa	aca		452
Ile	Leu	Ser	Cys	Leu	Gly	Leu	Ser	Ile	Val	Ala	Asn	Phe	Gln	Lys	Thr		
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acc	ctt	ttt	gct	gca	cat	gta	agt	gga	gct	gtg	ctt	acc	ttt	ggt	atg		500
Thr	Leu	Phe	Ala	Ala	His	Val	Ser	Gly	Ala	Val	Leu	Thr	Phe	Gly	Met		
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Gly	Ser	Leu	Tyr	Met	Phe	Val	Gln	Thr	Ile	Leu	Ser	Tyr	Gln	Met	Gln		
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ccc	aaa	atc	cat	ggc	aaa	caa	gtc	ttc	tgg	atc	aga	ctg	ttg	ttg	gtt		596
Pro	Lys	Ile	His	Gly	Lys	Gln	Val	Phe	Trp	Ile	Arg	Leu	Leu	Leu	Val		
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Ile	Trp	Cys	Gly	Val	Ser	Ala	Leu	Ser	Met	Leu	Thr	Cys	Ser	Ser	Val		
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Leu	His	Ser	Gly	Asn	Phe	Gly	Thr	Asp	Leu	Glu	Gln	Lys	Leu	His	Trp		
		160					165					170					
aac	ccc	gag	gac	aaa	ggg	tat	gcg	ctt	cac	atg	atc	act	act	gca	gca		740
Asn	Pro	Glu	Asp	Lys	Gly	Tyr	Ala	Leu	His	Met	Ile	Thr	Thr	Ala	Ala		
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gaa	tgg	tct	atg	tca	ttt	tcc	ttc	ttt	ggg	ttt	ttc	ctg	act	tac	att		788
Glu	Trp	Ser	Met	Ser	Phe	Ser	Phe	Phe	Gly	Phe	Phe	Leu	Thr	Tyr	Ile		
			195									200			205		
cgt	gat	ttt	cag	aaa	att	tcc	tta	cgg	gtg	gaa	gcc	aac	tta	cat	gga		836
Arg	Asp	Phe	Gln	Lys	Ile	Ser	Leu	Arg	Val	Glu	Ala	Asn	Leu	His	Gly		
			210						215				220				
tta	acc	ctc	tat	gac	act	gca	cct	tgc	cct	att	aac	aat	gaa	cga	aca		884
Leu	Thr	Leu	Tyr	Asp	Thr	Ala	Pro	Cys	Pro	Ile	Asn	Asn	Glu	Arg	Thr		
		225					230						235				
cgg	cta	ctt	tcc	aga	gat	att	aga	tgaaaggata	aaatatttct	gtaatgatta							938
Arg	Leu	Leu	Ser	Arg	Asp	Ile	Arg										
		240					245										
tgattctcag	ggattgggga	aaggttcaca	gaagttgctt	attcttctct	gaaattttca												998
accacttaat	caaggctgac	agtaacactg	atgaatgctg	ataatcagga	aacatgaaag												1058
aagccatttg	atagattatt	ctaaaggata	tcatcaagaa	gactattaaa	aacacctatg												1118
cctatacttt	tttatctcag	aaaataaagt	caaaagacta	tgaaaaaaa	aaaaaa												1174

<210> 144
 <211> 1158
 <212> DNA
 <213> Homo sapiens

<220>
 <221> polyA_signal
 <222> 1133..1138

 <221> polyA_site
 <222> 1146..1158

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<400> 144
aarttgagct tggggactgc agctgtgggg agatttcagt gcattgcctc ccctgggtgc      60
tcttcacatt ggatttgaaa gttgagagca gcatgttttg cccactgaaa ctcacctgcs    120
tgrsagtgtg mtggattatt ccttgggcct gaatgacttg aatgtttccc cgcctgagct    180
aacagtccat gtgggtgatt cagctctg atg gga tgt gtt ttc cag agc aca      232
                               Met Gly Cys Val Phe Gln Ser Thr
                               1           5
gaa gac aaa tgt ata ttc aag ata gac tgg act ctg tca cca gga gag      280
Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu
   10           15           20
cac gcc aag gac gaa tat gtg cta tac tat tac tcc aat ctc agt gtg      328
His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val
   25           30           35           40
cct att ggg cgc ttc cag aac cgc gta cac ttg atg ggg gac atc tta      376
Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Ile Leu
           45           50           55
tgc aat gat ggc tct ctc ctg ctc caa gat gtg caa gag gct gac cag      424
Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln
           60           65           70
gga acc tat atc tgt gaa atc cgc ctc aaa ggg gag agc cag gtg ttc      472
Gly Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe
           75           80           85
aag aag gcg gtg gta ctg cat gtg ctt cca gag gag ccc aaa ggt acg      520
Lys Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Gly Thr
           90           95          100
caa atg ctt act taaagagggg ccaaggggca agagctttca tgtgcaagag      572
Gln Met Leu Thr
105
gcaaggaaac tgattatctt gagtaaattgc cagccttttg gctaagtact taccacagag      632
tgaatcttca aagaaatgan tcattaaatt atttcagrtc agaataaaaa takgagttat      692
tttagttaak aataaaatat tgataattat tgtattatta ctttaaacac acttccccct      752
cacaaaagcc ctgtgaagga tgttttgctt acatataatg tccaaatatg ttttggacac      812
atatattatta aatggaataa atagtamttg aaccctggca ccthtgacaa caaagtcyat      872
gttyttttta ctatgcccta ataccttttsa tcagttatcc acattgatgc tacatytgta      932
ttttatagggt accctatgtt aggtgttttg ggggatagaa aagaaataag cagkycaggc      992
tcagtggtctc atgcctgtaa tcctagcatt ttgggaggct gaggcagcag aamtgcctga    1052
gccccagggt tcaagactgc agtgagctat gawggcacca ctgcattyta gcctgggwga    1112
cagagcaaga ctytgtttaa aataaaaaaa gagaaaaaaa aaaaaa                    1158

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<210> 145
<211> 754
<212> DNA
<213> Homo sapiens

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<220>
<221> sig_peptide
<222> 5..142
<223> Von Heijne matrix
      score 6.59999990463257
      seq VCCYLFWLIAILA/QL

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<221> polyA_signal
<222> 716..721

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<221> polyA_site
<222> 742..754

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<400> 145
tgtg atg agc gtg ttc tgg ggc ttc gtc ggc ttc ttg gtg cct tgg ttc      49
    Met Ser Val Phe Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe
        -45                -40                -35
atc ccc aag ggt cct aac cgg gga gtt atc att acc atg ttg gtg acc      97
Ile Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr
    -30                -25                -20
tgt tca gtt tgc tgc tat ctc ttt tgg ctg att gca att ctg gcc caa     145
Cys Ser Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln
    -15                -10                -5                1
ctc aac cct ctc ttt gga ccg caa ttg aaa aat gaa acc atc tgg tat     193
Leu Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr
        5                10                15
ctg aag tat cat tgg cct tgaggaagaa gacatgctct acagtgtctca         241
Leu Lys Tyr His Trp Pro
    20
gtcttttgagg tcacgagaag agaatgcctt ctagatgcaa aatcacctct aaaccagacc   301
acttttcttg acttgccctgt tttggccatt agctgcctta aacgttaaca gcacatttga   361
atgccttatt ctacaatgca gcgtgttttc ctttgccttt tttgcacttt ggtgaattac   421
gtgcctccat aacctgaact gtgccgactc cacaaaaacga ttatgtactc ttctgagata   481
gaagatgctg ttcttctgag agatacgtta ctctctcctt ggaatctgtg gatttgaaga   541
tggctcctgc cttctcacgt gggaatcagt gaagtgttta gaaactgctg caagacaaac   601
aagactccag tggggtggtc agtaggagag cacgttcaga gggaagagcc atctcaacag   661
aatcgacca aactatactt tcaggatgaa tttcttcttt ctgccatctt ttggaataaa   721
tattttcctc ctttctatgt aaaaaaaaaa aaa                                754

<210> 146
<211> 1073
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 98..181
<223> Von Heijne matrix
      score 3.59999990463257
      seq PLSDSWALLPASA/GV

<221> polyA_signal
<222> 1035..1040

<221> polyA_site
<222> 1060..1073

<400> 146
ccgattacag ctaggtagtg gagcgccgct gcttacctgg gtgcaggaga cagccggagt     60
cgctggggga gctccgcgcc gccggacgcc cgtgacc atg tgg agg ctg ctg gct     115
                                Met Trp Arg Leu Leu Ala
                                    -25
cgc gct agt gcg ccg ctc ctg cgg gtg ccc ttg tca gat tcc tgg gca     163
Arg Ala Ser Ala Pro Leu Leu Arg Val Pro Leu Ser Asp Ser Trp Ala
    -20                -15                -10
ctc ctc ccc gcc agt gct ggc gta aag aca ctg ctc cca gta cca agt     211
Leu Leu Pro Ala Ser Ala Gly Val Lys Thr Leu Leu Pro Val Pro Ser
    -5                1                5                10
ttt gaa gat gtt tcc att cct gaa aaa ccc aag ctt aga ttt att gaa     259

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Phe	Glu	Asp	Val	Ser	Ile	Pro	Glu	Lys	Pro	Lys	Leu	Arg	Phe	Ile	Glu		
				15					20					25			
agg	gca	cca	ctt	gtg	cca	aaa	gta	aga	aga	gaa	cct	aaa	aat	tta	agt	307	
Arg	Ala	Pro	Leu	Val	Pro	Lys	Val	Arg	Arg	Glu	Pro	Lys	Asn	Leu	Ser		
			30					35					40				
gac	ata	cgg	gga	cct	tcc	act	gaa	gct	acg	gag	ttt	aca	gaa	ggc	aat	355	
Asp	Ile	Arg	Gly	Pro	Ser	Thr	Glu	Ala	Thr	Glu	Phe	Thr	Glu	Gly	Asn		
			45				50					55					
ttt	gca	atc	ttg	gca	ttg	ggt	ggt	ggc	tac	ctg	cat	tgg	ggc	cac	ttt	403	
Phe	Ala	Ile	Leu	Ala	Leu	Gly	Gly	Gly	Tyr	Leu	His	Trp	Gly	His	Phe		
	60					65			70								
gaa	atg	atg	cgc	ctg	aca	atc	aac	cgc	tct	atg	gac	ccc	aag	aac	atg	451	
Glu	Met	Met	Arg	Leu	Thr	Ile	Asn	Arg	Ser	Met	Asp	Pro	Lys	Asn	Met		
	75				80				85					90			
ttt	gcc	ata	tgg	cga	gta	cca	gcc	cct	ttc	aag	ccc	atc	act	cgc	aaa	499	
Phe	Ala	Ile	Trp	Arg	Val	Pro	Ala	Pro	Phe	Lys	Pro	Ile	Thr	Arg	Lys		
			95					100					105				
agt	gtt	ggg	cat	cgc	atg	ggg	gga	ggc	aaa	ggt	gct	att	gac	cac	tac	547	
Ser	Val	Gly	His	Arg	Met	Gly	Gly	Gly	Lys	Gly	Ala	Ile	Asp	His	Tyr		
			110					115					120				
gtg	aca	cct	gtg	aag	gct	ggc	cgc	ctt	gtt	gta	gag	atg	ggt	ggg	cgt	595	
Val	Thr	Pro	Val	Lys	Ala	Gly	Arg	Leu	Val	Val	Glu	Met	Gly	Gly	Arg		
			125				130					135					
tgt	gaa	ttt	gaa	gaa	gtg	caa	ggt	ttc	ctt	gac	cag	gtt	gcc	cac	aag	643	
Cys	Glu	Phe	Glu	Glu	Val	Gln	Gly	Phe	Leu	Asp	Gln	Val	Ala	His	Lys		
			140			145					150						
ttg	ccc	ttc	gca	gca	aag	gct	gtg	agc	cgc	ggg	act	cta	gag	aag	atg	691	
Leu	Pro	Phe	Ala	Ala	Lys	Ala	Val	Ser	Arg	Gly	Thr	Leu	Glu	Lys	Met		
			155		160				165					170			
cga	aaa	gat	caa	gag	gaa	aga	gaa	cgt	aac	aac	cag	aac	ccc	tgg	aca	739	
Arg	Lys	Asp	Gln	Glu	Glu	Arg	Glu	Arg	Asn	Asn	Gln	Asn	Pro	Trp	Thr		
			175					180					185				
ttt	gag	cga	ata	gcc	act	gcc	aac	atg	ctg	ggc	ata	cgg	aaa	gta	ctg	787	
Phe	Glu	Arg	Ile	Ala	Thr	Ala	Asn	Met	Leu	Gly	Ile	Arg	Lys	Val	Leu		
			190					195					200				
agc	cca	tat	gac	ttg	acc	cac	aag	ggg	aaa	tac	tgg	ggc	aag	ttc	tac	835	
Ser	Pro	Tyr	Asp	Leu	Thr	His	Lys	Gly	Lys	Tyr	Trp	Gly	Lys	Phe	Tyr		
			205				210					215					
atg	ccc	aaa	cgt	gtg	tagtgagtgt	aggagataaac	tgtatataggt	ctactgaaag								890	
Met	Pro	Lys	Arg	Val													
			220														
aaggattctg	catttctatt	cccctcagcc	taccactga	agtcctttggg	tagctcttaa											950	
gccataacta	aggagcagca	tttgagtaga	tttctgaaaa	acgatgttat	ttgttgattt											1010	
aaaaagaaaa	ctgtattttt	attaaataaa	atttaaacad	cacttcagga	aaaaaaaaaa											1070	
aaa																1073	

<210> 147
 <211> 413
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 46..189
 <223> Von Heijne matrix
 score 4.09999990463257
 seq VFMLIVSVLALIP/ET

<221> polyA_signal
<222> 377..382

<221> polyA_site
<222> 402..413

<400> 147

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tgagaagagt tgagggaaag tgctgctgct gggctctgcag acgcg atg gat aac gtg      57
                                     Met Asp Asn Val
                                     -45
cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg aaa ggc cac      105
Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val Lys Gly His
          -40                      -35          -30
gtg aag atg ctg cgg ctg gat att atc aac tca ctg gta aca aca gta      153
Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val
          -25                      -20          -15
ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa acc aca aca      201
Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
          -10                      -5              1
ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca gta tgc tgc      249
Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys
5          10          15          20
ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc aat ccc agc      297
Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser
          25          30          35
ggg cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa gtt ttg      342
Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
          40          45          50
taattttata ttacttttta gtttgatact aagtattaaa catatttctg tattcttcca      402
aaaaaaaaaa a      413
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<210> 148
<211> 609
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 139..231
<223> Von Heijne matrix
score 4.40000009536743
seq TCCHLGLPHPVRA/PR

<221> polyA_signal
<222> 579..584

<221> polyA_site
<222> 598..609

<400> 148

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tgctcgagatt ggaaagggac gcctgggtttc cccccaagcg aaccgggatg ggaagtgact      60
tcaatgagat tgaacttcag ctggattgaa agagaggcta gaagttccgc ttgccagcag      120
cctccttagt agagcgga atg agt aat acc cac acg gtg ctt gtc tca ctt      171
          Met Ser Asn Thr His Thr Val Leu Val Ser Leu
          -30          -25
ccc cat ccg cac ccg gcc ctc acc tgc tgt cac ctc ggc ctc cca cac      219
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Pro His Pro His Pro Ala Leu Thr Cys Cys His Leu Gly Leu Pro His	
-20 -15 -10 -5	
ccg gtc cgc gct ccc cgc cct ctt cct cgc gta gaa ccg tgg gat cct	267
Pro Val Arg Ala Pro Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro	
1 5 10	
agg tgg cag gac tca gag cta agg tat cca cag gcc atg aat tcc ttc	315
Arg Trp Gln Asp Ser Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe	
15 20 25	
cta aat gag cgg tca tcg ccg tgc agg acc tta agg caa gaa gca tcg	363
Leu Asn Glu Arg Ser Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser	
30 35 40	
gct gac aga tgt gat ctc tgaacctgat agattgctga ttttatctta	411
Ala Asp Arg Cys Asp Leu	
45 50	
ttttatcctt gacttggtac aagttttggg atttctgaaa agaccataca gataaccaca	471
aatatcaaga aagtcgtctt cagtattaag tagaatttag atttaggttt ccttcctgct	531
tcccacctcc ttcgaataag gaaacgtctt tgggaccaac tttatggaat aaataagctg	591
agctgcacaaa aaaaaaaaa	609

<210> 149
 <211> 522
 <212> DNA
 <213> Homo sapiens

<220>
 <221> polyA_site
 <222> 512..522

<400> 149

ccaactgcag nttcgaatth accgagcgga gaggagatgc acacggcact cgagtgtgag	60
gaaaaataga a atg aag gta cat atg cac aca aaa ttt tgc ctc att tgt	110
Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys	
1 5 10	
ttg ctg aca ttt att ttt cat cat tgc aac cat tgc cat gaa gaa cat	158
Leu Leu Thr Phe Ile Phe His His Cys Asn His Cys His Glu Glu His	
15 20 25	
gac cat ggc cct gaa gcg ctt cac aga cag cat cgt gga atg aca gaa	206
Asp His Gly Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu	
30 35 40 45	
ttg gag cca agc aaa ttt tca aag caa gct gct gaa aat gaa aaa aaa	254
Leu Glu Pro Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys	
50 55 60	
tac tat att gaa aaa ctt ttt gag cgt tat ggt gaa aat gga aga tta	302
Tyr Tyr Ile Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu	
65 70 75	
tcc ttt ttt ggt ttg gag aaa ctt tta aca aac ttg ggc ctt gga gag	350
Ser Phe Phe Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu	
80 85 90	
aga aaa gta gtt gag att aat cat gag gat ctt ggc cac gat cat gtt	398
Arg Lys Val Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val	
95 100 105	
tct cat tta ggt att ttg gca gtt caa gag gga aag cat ttt cac tca	446
Ser His Leu Gly Ile Leu Ala Val Gln Glu Gly Lys His Phe His Ser	
110 115 120 125	
cat aac cac cag cat tcc cat aat cat tta aat tca gaa aat caa act	494
His Asn His Gln His Ser His Asn His Leu Asn Ser Glu Asn Gln Thr	
130 135 140	

gtg acc agt gta tcc aca aaaaaaaaaa
 Val Thr Ser Val Ser Thr
 145

522

<210> 150
 <211> 1322
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 126..260
 <223> Von Heijne matrix
 score 4.59999990463257
 seq VLVYLVTAERVWS/DD

<221> polyA_signal
 <222> 1283..1288

<221> polyA_site
 <222> 1309..1322

<400> 150
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 gctgctggga gccaggagag ccctgaggag tagtcactca gtagcagctg acgcgtgggt 120
 ccacc atg aac tgg agt atc ttt gag gga ctc ctg agt ggg gtc aac aag 170
 Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys
 -45 -40 -35
 tac tcc aca gcc ttt ggg cgc atc tgg ctg tct ctg gtc ttc atc ttc 218
 Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe
 -30 -25 -20 -15
 cgc gtg ctg gtg tac ctg gtg acg gcc gag cgt gtg tgg agt gat gac 266
 Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp
 -10 -5 1
 cac aag gac ttc gac tgc aat act cgc cag ccc ggc tgc tcc aac gtc 314
 His Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val
 5 10 15
 tgc ttt gat gag ttc ttc cct gtg tcc cat gtg cgc ctc tgg gcc ctg 362
 Cys Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu
 20 25 30
 cag ctt atc ctg gtg aca tgc ccc tca ctg ctc gtg gtc atg cac gtg 410
 Gln Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val
 35 40 45 50
 gcc tac cgg gag gtt cag gag aag agg cac cga gaa gcc cat ggg gag 458
 Ala Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu
 55 60 65
 aac agt ggg cgc ctc tac ctg aac ccc ggc aag aag cgg ggt ggg ctc 506
 Asn Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu
 70 75 80
 tgg tgg aca tat gtc tgc agc cta gtg ttc aag gcg agc gtg gac atc 554
 Trp Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile
 85 90 95
 gcc ttt ctc tat gtg ttc cac tca ttc tac ccc aaa tat atc ctc cct 602
 Ala Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro
 100 105 110
 cct gtg gtc aag tgc cac gca gat cca tgt ccc aat ata gtg gac tgc 650
 Pro Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys

115	120	125	130	
ttc atc tcc aag ccc tca gag aag aac att ttc acc ctc ttc atg gtg				698
Phe Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val				
	135	140	145	
gcc aca gct gcc atc tgc atc ctg ctc aac ctc gtg gag ctc atc tac				746
Ala Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr				
	150	155	160	
ctg gtg agc aag aga tgc cac gag tgc ctg gca gca agg aaa gct caa				794
Leu Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln				
	165	170	175	
gcc atg tgc aca ggt cat cac ccc cac gat acc acc tct tcc tgc aaa				842
Ala Met Cys Thr Gly His His Pro His Asp Thr Thr Ser Ser Cys Lys				
	180	185	190	
caa gac gac ctc ctt tcg ggt gac ctc atc ttt ctg ggc tca gac agt				890
Gln Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser				
	195	200	205	210
cat cct cct ctc tta cca gac cgc ccc cga gac cat gtg aag aaa acc				938
His Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr				
	215	220	225	
atc ttg tgaggggctg cctggactgg tctggcaggt tgggcctgga tggggaggct				994
Ile Leu				
ctagcatctc tcataggtgc aacctgagag tgggggagct aagccatgag gtaggggcag				1054
gcaagagaga ggattcagac gctctgggag ccagttccta gtcctcaact ccagccacct				1114
gccccagctc gacggcactg ggccagttcc ccctctgctc tgcagctcgg ttctcttttc				1174
tagaatggaa atagtgaggg ccaatgcccc gggttgaggg gaggagggcg ttcatagaag				1234
aacacacatg cgggcacctt catcgtgtgt ggcccaactgt cagaacttaa taaaagtcaa				1294
ctcatttgcg ggttaaaaaa aaaaaaaa				1322

<210> 151
 <211> 1290
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> sig_peptide
 <222> 50..160
 <223> Von Heijne matrix
 score 4
 seq PLSLDCGHS LCRA/CI

<221> polyA_site
 <222> 1280..1290

<400> 151	
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	Met Ala Ser
	-35
aaa atc ttg ctt aac gta caa gag gag gtg acc tgt ccc atc tgc ctg	106
Lys Ile Leu Leu Asn Val Gln Glu Glu Val Thr Cys Pro Ile Cys Leu	
	-30 -25 -20
gag ctg ttg aca gaa ccc ttg agt cta gac tgt ggc cac agc ctc tgc	154
Glu Leu Leu Thr Glu Pro Leu Ser Leu Asp Cys Gly His Ser Leu Cys	
	-15 -10 -5
cga gcc tgc atc act gtg agc aac aag gag gca gtg acc agc atg gga	202
Arg Ala Cys Ile Thr Val Ser Asn Lys Glu Ala Val Thr Ser Met Gly	
	1 5 10
gga aaa agc agc tgt cct gtg tgt ggt atc agt tac tca ttt gaa cat	250

Gly 15	Lys	Ser	Ser	Cys	Pro 20	Val	Cys	Gly	Ile	Ser 25	Tyr	Ser	Phe	Glu	His 30	
cta	cag	gct	aat	cag	cat	ctg	gcc	aac	ata	gtg	gag	aga	ctc	aag	gag	298
Leu	Gln	Ala	Asn	Gln	His	Leu	Ala	Asn	Ile	Val	Glu	Arg	Leu	Lys	Glu	
				35					40					45		
gtc	aag	ttg	agc	cca	gac	aat	ggg	aag	aag	aga	gat	ctc	tgt	gat	cat	346
Val	Lys	Leu	Ser	Pro	Asp	Asn	Gly	Lys	Lys	Arg	Asp	Leu	Cys	Asp	His	
			50					55					60			
cat	gga	gag	aaa	ctc	cta	ctc	ttc	tgt	aag	gag	gat	agg	aaa	gtc	att	394
His	Gly	Glu	Lys	Leu	Leu	Leu	Phe	Cys	Lys	Glu	Asp	Arg	Lys	Val	Ile	
			65				70					75				
tgc	tgg	ctt	tgt	gag	cgg	tct	cag	gag	cac	cgt	ggg	cac	cac	aca	gtc	442
Cys	Trp	Leu	Cys	Glu	Arg	Ser	Gln	Glu	His	Arg	Gly	His	His	Thr	Val	
	80					85					90					
ctc	acg	gag	gaa	gta	ttc	aag	gaa	tgt	cag	gag	aaa	ctc	cag	gca	gtc	490
Leu	Thr	Glu	Glu	Val	Phe	Lys	Glu	Cys	Gln	Glu	Lys	Leu	Gln	Ala	Val	
					100						105				110	
ctc	aag	agg	ctg	aag	aag	gaa	gag	gag	gaa	gct	gag	aag	ctg	gaa	gct	538
Leu	Lys	Arg	Leu	Lys	Lys	Glu	Glu	Glu	Glu	Ala	Glu	Lys	Leu	Glu	Ala	
				115					120					125		
gac	atc	aga	gaa	gag	aaa	act	tcc	tgg	aag	tat	cag	gta	caa	act	gag	586
Asp	Ile	Arg	Glu	Glu	Lys	Thr	Ser	Trp	Lys	Tyr	Gln	Val	Gln	Thr	Glu	
			130					135					140			
aga	caa	agg	ata	caa	aca	gaa	ttt	gat	cag	ctt	aga	agc	atc	cta	aat	634
Arg	Gln	Arg	Ile	Gln	Thr	Glu	Phe	Asp	Gln	Leu	Arg	Ser	Ile	Leu	Asn	
			145				150					155				
aat	gag	gag	cag	aga	gag	ctg	caa	aga	ttg	gaa	gaa	gaa	gaa	aag	aag	682
Asn	Glu	Glu	Gln	Arg	Glu	Leu	Gln	Arg	Leu	Glu	Glu	Glu	Glu	Lys	Lys	
			160			165				170						
acg	ctg	gat	aag	ttt	gca	gag	gct	gag	gat	gag	cta	gtt	cag	cag	aag	730
Thr	Leu	Asp	Lys	Phe	Ala	Glu	Ala	Glu	Asp	Glu	Leu	Val	Gln	Gln	Lys	
				175		180			185						190	
cag	ttg	gtg	aga	gag	ctc	atc	tca	gat	gtg	gag	tgt	cgg	agt	cag	tgg	778
Gln	Leu	Val	Arg	Glu	Leu	Ile	Ser	Asp	Val	Glu	Cys	Arg	Ser	Gln	Trp	
				195				200						205		
tca	aca	atg	gag	ctg	ctg	cag	gac	atg	agt	gga	atc	atg	aaa	tgg	agt	826
Ser	Thr	Met	Glu	Leu	Leu	Gln	Asp	Met	Ser	Gly	Ile	Met	Lys	Trp	Ser	
			210				215					220				
gag	atc	tgg	agg	ctg	aaa	aag	cca	aaa	atg	gtt	tcc	aag	aaa	ctg	aag	874
Glu	Ile	Trp	Arg	Leu	Lys	Lys	Pro	Lys	Met	Val	Ser	Lys	Lys	Leu	Lys	
			225				230				235					
act	gta	ttc	cat	gct	cca	gat	ctg	agt	agg	atg	ctg	caa	atg	ttt	aga	922
Thr	Val	Phe	His	Ala	Pro	Asp	Leu	Ser	Arg	Met	Leu	Gln	Met	Phe	Arg	
			240			245					250					
gaa	ctg	aca	gct	gtc	cgg	tgc	tac	tgg	gtg	gat	gtc	aca	ctg	aat	tca	970
Glu	Leu	Thr	Ala	Val	Arg	Cys	Tyr	Trp	Val	Asp	Val	Thr	Leu	Asn	Ser	
			255			260				265					270	
gtc	aac	cta	aat	ttg	aat	ctt	gtc	ctt	tca	gaa	gat	cag	aga	caa	gtg	1018
Val	Asn	Leu	Asn	Leu	Asn	Leu	Val	Leu	Ser	Glu	Asp	Gln	Arg	Gln	Val	
				275				280						285		
ata	tct	gtg	cca	att	tgg	cct	ttt	cag	tgt	tat	aat	tat	ggg	gtc	ttg	1066
Ile	Ser	Val	Pro	Ile	Trp	Pro	Phe	Gln	Cys	Tyr	Asn	Tyr	Gly	Val	Leu	
			290				295						300			
gga	tcc	caa	tat	ttc	tcc	tct	ggg	aaa	cat	tac	tgg	gaa	gtg	gac	gtg	1114
Gly	Ser	Gln	Tyr	Phe	Ser	Ser	Gly	Lys	His	Tyr	Trp	Glu	Val	Asp	Val	
			305				310					315				
tcc	aag	aaa	act	gcc	tgg	atc	ctg	ggg	gta	tac	tgt	aga	aca	tat	tcc	1162
Ser	Lys	Lys	Thr	Ala	Trp	Ile	Leu	Gly	Val	Tyr	Cys	Arg	Thr	Tyr	Ser	

320	325	330	
cgc cat atg aag tat gtt gtt aga aga tgt gca aat cgt caa aat ctt			1210
Arg His Met Lys Tyr Val Val Arg Arg Cys Ala Asn Arg Gln Asn Leu			
335	340	345	350
tac acc aaa tac aga cct cta ttt ggc tac tgg gtt ata ggg tta cag			1258
Tyr Thr Lys Tyr Arg Pro Leu Phe Gly Tyr Trp Val Ile Gly Leu Gln			
	355	360	365
aat aaa tgt aag tat ggt gcc aaaaaaaaa a			1290
Asn Lys Cys Lys Tyr Gly Ala			
370			

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 <211> 1364
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 83..139
 <223> Von Heijne matrix
 score 8.60000038146973
 seq LLWLALACSPVHT/TL

<221> polyA_site
 <222> 1356..1354

<400> 152

gcctgggagc tgaggcagcc accgtctcag cctggccagc cctctggacc ccgaggttgg	60
accctactgt gacacaccta cc atg cgg aca ctc ttc aac ctc ctc tgg ctt	112
Met Arg Thr Leu Phe Asn Leu Leu Trp Leu	
-15	-10
gcc ctg gcc tgc agc cct gtt cac act acc ctg tca aag tca gat gcc	160
Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala	
-5	1
5	
aaa aaa gcc gcc tca aag acg ctg ctg gag aag agt cag ttt tca gat	208
Lys Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp	
10	15
20	
aag ccg gtg caa gac cgg ggt ttg gtg gtg acg gac ctc aaa gct gag	256
Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu	
25	30
35	
agt gtg gtt ctt gag cat cgc agc tac tgc tgc gca aag gcc cgg gac	304
Ser Val Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp	
40	45
50	55
aga cac ttt gct ggg gat gta ctg ggc tat gtc act cca tgg aac agc	352
Arg His Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser	
60	65
70	
cat ggc tac gat gtc acc aag gtc ttt ggg agc aag ttc aca cag atc	400
His Gly Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile	
75	80
85	
tca ccc gtc tgg ctg cag ttg aag aga cgt ggc cgt gag atg ttt gag	448
Ser Pro Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu	
90	95
100	
gtc acg ggc ctc cac gac gtg gac caa ggg tgg atg cga gct gtc agg	496
Val Thr Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg	
105	110
115	
aag cat gcc aag ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac	544
Lys His Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp	

120	125	130	135	
tgg act tac gat gat ttc cgg aac gtc tta gac agt gag gat gag ata				592
Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile				
	140	145	150	
gag gag ctg agc aag acc gtg gtc cag gtg gca aag aac cag cat ttc				640
Glu Glu Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe				
	155	160	165	
gat ggc ttc gtg gtg gag gtc tgg aac cag ctg cta agc cag aag cgc				688
Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg				
	170	175	180	
gtg ggc ctc atc cac atg ctc acc cac ttg gcc gag gcc ctg cac cag				736
Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln				
	185	190	195	
gcc cgg ctg ctg gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg				784
Ala Arg Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly				
200	205	210	215	
acc gac cag ctg ggc atg ttc acg cac aag gag ttt gag cag ctg gcc				832
Thr Asp Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala				
	220	225	230	
ccc gtg ctg gat ggt ttc agc ctc atg acc tac gac tac tct aca gcg				880
Pro Val Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala				
	235	240	245	
cat cag cct ggc cct aat gca ccc ctg tcc tgg gtt cga gcc tgc gtc				928
His Gln Pro Gly Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val				
	250	255	260	
cag gtc ctg gac ccg aag tcc aag tgg cga agc aaa atc ctc ctg ggg				976
Gln Val Leu Asp Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly				
	265	270	275	
ctc aac ttc tat ggt atg gac tac gcg acc tcc aag gat gcc cgt gag				1024
Leu Asn Phe Tyr Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu				
	280	285	290	
cct gtt gtc ggg gcc agg tac atc cag aca ctg aag gac cac agg ccc				1072
Pro Val Val Gly Ala Arg Tyr Ile Gln Thr Leu Lys Asp His Arg Pro				
	300	305	310	
cgg atg gtg tgg gac agc cag gcc tca gag cac ttc ttc gag tac aag				1120
Arg Met Val Trp Asp Ser Gln Ala Ser Glu His Phe Phe Glu Tyr Lys				
	315	320	325	
aag agc cgc agt ggg agg cac gtc gtc ttc tac cca acc ctg aag tcc				1168
Lys Ser Arg Ser Gly Arg His Val Val Phe Tyr Pro Thr Leu Lys Ser				
	330	335	340	
ctg cag gtg cgg ctg gag ctg gcc cgg gag ctg ggc gtt ggg gtc tct				1216
Leu Gln Val Arg Leu Glu Leu Ala Arg Glu Leu Gly Val Gly Val Ser				
	345	350	355	
atc tgg gag ctg ggc cag ggc ctg gac tac ttc tac gac ctg ctc				1261
Ile Trp Glu Leu Gly Gln Gly Leu Asp Tyr Phe Tyr Asp Leu Leu				
	360	365	370	
taggtgggca ttgcggcctc cgcggtggac gtgttctttt ctaagccatg gagtgagtga				1321
gcaggtgtga aatacaggcc tccactccgt ttgcaaaaaa aaa				1364

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<223> Von Heijne matrix
 score 3.90000009536743
 seq MLLSIGMLMLSAT/QV

<221> polyA_signal
 <222> 1438..1443

<221> polyA_site
 <222> 1458..1470

<400> 153

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	Met
ctg ctc tcc ata ggg atg ctc atg ctg tca gcc aca caa gtc tac acc	107
Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr Thr	
-10 -5 1	
gtc ttg act gtc cag ctc ttt gca ttc tta aac cca ctg cct gta gaa	155
Val Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Pro Leu Pro Val Glu	
5 10 15 20	
gca gac att tta gca tat aac ttt gaa aat gca tct cag aca ttt gat	203
Ala Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe Asp	
25 30 35	
gac ctc cct gca aga ttt ggt tat aga ctt cca gct gaa ggt tta aag	251
Asp Leu Pro Ala Arg Phe Gly Tyr Arg Leu Pro Ala Glu Gly Leu Lys	
40 45 50	
ggg ttt tta att aac tca aaa cca gag aat gcc tgt gaa ccc ata gtg	299
Gly Phe Leu Ile Asn Ser Lys Pro Glu Asn Ala Cys Glu Pro Ile Val	
55 60 65	
cct cca cca gta aaa gac aat tca tct ggc act ttc atc gtg tta att	347
Pro Pro Pro Val Lys Asp Asn Ser Ser Gly Thr Phe Ile Val Leu Ile	
70 75 80	
aga aga ctt gat tgt aat ttt gat ata aag gtt tta aat gca cag aga	395
Arg Arg Leu Asp Cys Asn Phe Asp Ile Lys Val Leu Asn Ala Gln Arg	
85 90 95 100	
gca gga tac aag gca gcc ata gtt cac aat gtt gat tct gat gac ctc	443
Ala Gly Tyr Lys Ala Ala Ile Val His Asn Val Asp Ser Asp Asp Leu	
105 110 115	
att agc atg gga tcc aac gac att gag gta cta aag aaa att gac att	491
Ile Ser Met Gly Ser Asn Asp Ile Glu Val Leu Lys Lys Ile Asp Ile	
120 125 130	
cca tct gtc ttt att ggt gaa tca tca gct agt tct ctg aaa gat gaa	539
Pro Ser Val Phe Ile Gly Glu Ser Ser Ala Ser Ser Leu Lys Asp Glu	
135 140 145	
ttc aca tat gaa aaa ggg ggc cac ctt atc tta gtt cca gaa ttt agt	587
Phe Thr Tyr Glu Lys Gly Gly His Leu Ile Leu Val Pro Glu Phe Ser	
150 155 160	
ctt cct ttg gaa tac tac cta att ccc ttc ctt atc ata gtg ggc atc	635
Leu Pro Leu Glu Tyr Tyr Leu Ile Pro Phe Leu Ile Ile Val Gly Ile	
165 170 175 180	
tgt ctc atc ttg ata gtc att ttc atg atc aca aaa ttt gtc cag gat	683
Cys Leu Ile Leu Ile Val Ile Phe Met Ile Thr Lys Phe Val Gln Asp	
185 190 195	
aga cat aga gct aga aga aac aga ctt cgt aaa gat caa ctt aag aaa	731
Arg His Arg Ala Arg Arg Asn Arg Leu Arg Lys Asp Gln Leu Lys Lys	
200 205 210	
ctt cct gta cat aaa ttc aag aaa gga gat gag tat gat gta tgt gcc	779
Leu Pro Val His Lys Phe Lys Lys Gly Asp Glu Tyr Asp Val Cys Ala	
215 220 225	

att tgt ttg gat gag tat gaa gat gga gac aaa ctc aga atc ctt ccc	827
Ile Cys Leu Asp Glu Tyr Glu Asp Gly Asp Lys Leu Arg Ile Leu Pro	
230 235 240	
tgt tcc cat gct tat cat tgc aag tgt gta gac cct-tgg cta act aaa	875
Cys Ser His Ala Tyr His Cys Lys Cys Val Asp Pro Trp Leu Thr Lys	
245 250 255 260	
acc aaa aaa acc tgt cca gtg tgc agg caa aaa gtt gtt cct tct caa	923
Thr Lys Lys Thr Cys Pro Val Cys Arg Gln Lys Val Val Pro Ser Gln	
265 270 275	
ggc gat tca gac tct gac aca gac agt agt caa gaa gaa aat gaa gtg	971
Gly Asp Ser Asp Ser Asp Thr Asp Ser Ser Gln Glu Glu Asn Glu Val	
280 285 290	
aca gaa cat acc cct tta ctg aga cct tta gct tct gtc agt gcc cag	1019
Thr Glu His Thr Pro Leu Leu Arg Pro Leu Ala Ser Val Ser Ala Gln	
295 300 305	
tca ttt ggg gct tta tcg gaa tcc cgc tca cat cag aac atg aca gaa	1067
Ser Phe Gly Ala Leu Ser Glu Ser Arg Ser His Gln Asn Met Thr Glu	
310 315 320	
tct tca gac tat gag gaa gac gac aat gaa gat act gac agt agt gat	1115
Ser Ser Asp Tyr Glu Glu Asp Asp Asn Glu Asp Thr Asp Ser Ser Asp	
325 330 335 340	
gca gaa aat gaa att aat gaa cat gat gtc gtg gtc cag ttg cag cct	1163
Ala Glu Asn Glu Ile Asn Glu His Asp Val Val Val Gln Leu Gln Pro	
345 350 355	
aat ggt gaa cgg gat tac aac ata gca aat act gtt tgactttcag	1209
Asn Gly Glu Arg Asp Tyr Asn Ile Ala Asn Thr Val	
360 365	
aaagatgattg gtttatttcc ctttaaaatg attaggtata tactgtaatt tgattttttg	1269
ctcccttaaa agattttctgt agaaataact tatttttttag tactctacag tttaatcaaa	1329
ttactgaaac aggacttttg atctgggtatt tatctgccaa gaataatactt cattcactaa	1389
taatagactg gtgctgtaac tcaagcatca attcagctct tcttttgaa tgaaagtata	1449
gccaaaacaa aaaaaaaaaa a	1470

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 <211> 982
 <212> DNA
 <213> Homo sapiens

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 <221> sig_peptide
 <222> 72..197
 <223> Von Heijne matrix
 score 7.19999980926514
 seq ILFSLSFLLLVIIT/FP

<221> polyA_site
 <222> 970..982

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tcaagaatga g atg gat tct agg gtg tct tca cct gag aag caa gat aaa	110
Met Asp Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys	
-40 -35 -30	
gag aat ttc gtg ggt gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg	158
Glu Asn Phe Val Gly Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp	
-25 -20 -15	
atc ctg ttt tcc ctc tct ttc ctg ttg gtg atc att acc ttc ccc atc	206

Ile	Leu	Phe	Ser	Leu	Ser	Phe	Leu	Leu	Val	Ile	Ile	Thr	Phe	Pro	Ile		
			-10				-5						1				
tcc	ata	tgg	atg	tgc	ttg	aag	atc	att	agg	gag	tat	gaa	cgt	gct	gtt	254	
Ser	Ile	Trp	Met	Cys	Leu	Lys	Ile	Ile	Arg	Glu	Tyr	Glu	Arg	Ala	Val		
5						10					15						
gta	ttc	cgt	ctg	gga	cgc	atc	caa	gct	gac	aaa	gcc	aag	ggg	cca	ggt	302	
Val	Phe	Arg	Leu	Gly	Arg	Ile	Gln	Ala	Asp	Lys	Ala	Lys	Gly	Pro	Gly		
20					25				30						35		
ttg	atc	ctg	gtc	ctg	cca	tgc	ata	gat	gtg	ttt	gtc	aag	gtt	gac	ctc	350	
Leu	Ile	Leu	Val	Leu	Pro	Cys	Ile	Asp	Val	Phe	Val	Lys	Val	Asp	Leu		
			40						45					50			
cga	aca	gtt	act	tgc	aac	att	cct	cca	caa	gag	atc	ctc	acc	aga	gac	398	
Arg	Thr	Val	Thr	Cys	Asn	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Arg	Asp		
			55					60						65			
tcc	gta	act	act	cag	gta	gat	gga	gtt	gtc	tat	tac	aga	atc	tat	agt	446	
Ser	Val	Thr	Thr	Gln	Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Ile	Tyr	Ser		
			70				75					80					
gct	gtc	tca	gca	gtg	gct	aat	gtc	aac	gat	gtc	cat	caa	gca	aca	ttt	494	
Ala	Val	Ser	Ala	Val	Ala	Asn	Val	Asn	Asp	Val	His	Gln	Ala	Thr	Phe		
			85			90					95						
ctg	ctg	gct	caa	acc	act	ctg	aga	aat	gtc	tta	ggg	aca	cag	acc	ttg	542	
Leu	Leu	Ala	Gln	Thr	Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Gln	Thr	Leu		
100						105					110				115		
tcc	cag	atc	tta	gct	gga	cga	gaa	gag	atc	gcc	cat	agc	atc	cag	act	590	
Ser	Gln	Ile	Leu	Ala	Gly	Arg	Glu	Glu	Ile	Ala	His	Ser	Ile	Gln	Thr		
			120						125					130			
tta	ctt	gat	gat	gcc	acc	gaa	ctg	tgg	ggg	atc	cgg	gtg	gcc	cga	gtg	638	
Leu	Leu	Asp	Asp	Ala	Thr	Glu	Leu	Trp	Gly	Ile	Arg	Val	Ala	Arg	Val		
			135					140						145			
gaa	atc	aaa	gat	gtt	cgg	att	ccc	gtg	cag	ttg	cag	aga	tcc	atg	gca	686	
Glu	Ile	Lys	Asp	Val	Arg	Ile	Pro	Val	Gln	Leu	Gln	Arg	Ser	Met	Ala		
			150				155						160				
gcc	gag	gct	gag	gcc	acc	cgg	gaa	gcg	aga	gcc	aag	gtc	ctt	gca	gct	734	
Ala	Glu	Ala	Glu	Ala	Thr	Arg	Glu	Ala	Arg	Ala	Lys	Val	Leu	Ala	Ala		
			165				170					175					
gaa	gga	gaa	atg	agt	gct	tcc	aaa	tcc	ctg	aag	tca	gcc	tcc	atg	gtg	782	
Glu	Gly	Glu	Met	Ser	Ala	Ser	Lys	Ser	Leu	Lys	Ser	Ala	Ser	Met	Val		
180					185					190					195		
ctg	gct	gag	tct	ccc	ata	gct	ctc	cag	ctg	cgc	tac	ctg	cag	acc	ttg	830	
Leu	Ala	Glu	Ser	Pro	Ile	Ala	Leu	Gln	Leu	Arg	Tyr	Leu	Gln	Thr	Leu		
			200						205					210			
agc	acg	gta	gcc	acc	gag	aag	aat	tct	acg	att	gtg	ttt	cct	ctg	ccc	878	
Ser	Thr	Val	Ala	Thr	Glu	Lys	Asn	Ser	Thr	Ile	Val	Phe	Pro	Leu	Pro		
			215					220					225				
atg	aat	ata	cta	gag	ggc	att	ggt	ggc	gtc	agc	tat	gat	aac	cac	aag	926	
Met	Asn	Ile	Leu	Glu	Gly	Ile	Gly	Gly	Val	Ser	Tyr	Asp	Asn	His	Lys		
			230				235						240				
aag	ctt	cca	aat	aaa	gcc	tgagg	tcctc	ttgcg	gtagt	cagct	aaaaa	aaaaaaaa				982	
Lys	Leu	Pro	Asn	Lys	Ala												
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<210> 155
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 <213> Homo sapiens

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<221> polyA_signal
<222> 425..430

<221> polyA_site
<222> 443..455

<400> 155

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Met	Pro	Pro	Arg	Asn	Leu	Leu	Glu	Leu	Leu	Ile	Asn	Ile	Lys	Ala		
1				5				10						15		
gga	acc	tat	ttg	cct	cag	tcc	tat	ctg	att	cat	gag	cac	atg	ggt	att	96
Gly	Thr	Tyr	Leu	Pro	Gln	Ser	Tyr	Leu	Ile	His	Glu	His	Met	Val	Ile	
			20					25						30		
act	gat	cgc	atc	gaa	aac	att	gat	cac	ctg	ggt	ttc	ttt	att	tat	cga	144
Thr	Asp	Arg	Ile	Glu	Asn	Ile	Asp	His	Leu	Gly	Phe	Phe	Ile	Tyr	Arg	
			35					40						45		
ctg	tgt	cat	gac	aag	gaa	act	tac	aaa	ctg	caa	cgc	aga	gaa	act	att	192
Leu	Cys	His	Asp	Lys	Glu	Thr	Tyr	Lys	Leu	Gln	Arg	Arg	Glu	Thr	Ile	
			50					55						60		
aaa	ggt	att	cag	aaa	cgt	gaa	gcc	agc	aat	tgt	ttc	gca	att	cgg	cat	240
Lys	Gly	Ile	Gln	Lys	Arg	Glu	Ala	Ser	Asn	Cys	Phe	Ala	Ile	Arg	His	
			65					70						75		
ttt	gaa	aac	aaa	ttt	gcc	gtg	gaa	act	tta	att	tgt	tct	tgaacagtca			289
Phe	Glu	Asn	Lys	Phe	Ala	Val	Glu	Thr	Leu	Ile	Cys	Ser				
			80					85						90		
agaaaaacat	tattgaggaa	aattaatatc	acagcataac	cccacccttt	acattttgtg											349
cagtgtattat	tttttaaagt	cttctttcat	gtaagtagca	aacagggttt	tactatcttt											409
tcattctcatt	aattcaatta	aaaccattac	ccccaaaaaa	aaaaaa												455

<210> 156

<211> 738

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 90..278

<223> Von Heijne matrix

score 3.5

seq GLVCAGLADMARPAE

<221> polyA_signal

<222> 704..709

<221> polyA_site

<222> 724..738

<400> 156

gggaaaagtg	actagctccc	cttcgttgtc	agccagggtg	gagaacacag	ccacgtcccc	60		
accgggtg	caacgatccc	tcggcggtg	atg tgc gcc	gcc ggt gcc	cga ggc	113		
			Met Ser Ala	Ala Gly Ala	Arg Gly			
				-60				
ctg cgg gcc	acc tac cac	cgg ctc	ccc gat	aaa gtg	gag ctg	atg ctg	161	
Leu Arg Ala	Thr Tyr His	Arg Leu	Pro Asp	Lys Val	Glu Leu	Met Leu		
-55		-50		-45		-40		
ccc gag	aaa ttg	agg ccg	ttg tac	aac cat	cca gca	ggt ccc	aga aca	209
Pro Glu	Lys Leu	Arg Pro	Leu Tyr	Asn His	Pro Ala	Gly Pro	Arg Thr	

Ile	Asn	Pro	Asp	Gly	Ser	Gln	Ser	Val	Val	Glu	Val	Thr	Val	Thr	Val	
	40						45					50				
ccc	cca	aac	aaa	gta	gct	cac	tct	ggc	ttt	gga	tgaaaattcga	ctgcttaaaa				359
Pro	Pro	Asn	Lys	Val	Ala	His	Ser	Gly	Phe	Gly						
	55						60									
aggaccttgg	tctaatagaa	atgaagaaaa	cagactcaga	aaaaagattt	ggctctgtct											419
catttggaag	aagctgcagg	cttattcccc	atgcacttgc	ttcctggctg	caaacccttaa											479
tactttgttt	ctgctgtaga	atttgtttagc	aaacagggag	tcctgatcag	cacccttctc											539
cacatccaca	tgactggttt	ttaatgtagc	actgtggtat	acatgcaaac	atccgttcaa											599
aatctgagtc	ggagctaaaa	ataaaaaaatg	aaaaaacaaa	aaaaaaaaaa												649

<210> 158
 <211> 714
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 33..92
 <223> Von Heijne matrix
 score 12.39999996185303
 seq ALLLGALLGTAWA/RR

<221> polyA_site
 <222> 703..714

<400> 158																
agcagaggtg	gagcgacccc	attacgctaa	ag	atg	aaa	ggc	tgg	ggt	tgg	ctg						53
				Met	Lys	Gly	Trp	Gly	Trp	Leu						
				-20						-15						
gcc	ctg	ctt	ctg	ggg	gcc	ctg	ctg	gga	acc	gcc	tgg	gct	cgg	agg	agc	101
Ala	Leu	Leu	Leu	Gly	Ala	Leu	Leu	Gly	Thr	Ala	Trp	Ala	Arg	Arg	Ser	
				-10				-5					1			
cag	gat	ctc	cac	tgt	gga	gca	tgc	agg	gct	ctg	gtg	gat	gaa	cta	gaa	149
Gln	Asp	Leu	His	Cys	Gly	Ala	Cys	Arg	Ala	Leu	Val	Asp	Glu	Leu	Glu	
	5				10					15						
tgg	gaa	att	gcc	cag	gtg	gac	ccc	aag	aag	acc	att	cag	atg	gga	tct	197
Trp	Glu	Ile	Ala	Gln	Val	Asp	Pro	Lys	Lys	Thr	Ile	Gln	Met	Gly	Ser	
	20			25				30						35		
ttc	cgg	atc	aat	cca	gat	ggc	agc	cag	tca	gtg	gtg	gag	gtg	cct	tat	245
Phe	Arg	Ile	Asn	Pro	Asp	Gly	Ser	Gln	Ser	Val	Val	Glu	Val	Pro	Tyr	
			40					45						50		
gcc	cgc	tca	gag	gcc	cac	ctc	aca	gag	ctg	ctg	gag	gag	ata	tgt	gac	293
Ala	Arg	Ser	Glu	Ala	His	Leu	Thr	Glu	Leu	Glu	Glu	Ile	Cys	Asp		
			55					60					65			
cgg	atg	aag	gag	tat	ggg	gaa	cag	att	gat	cct	tcc	acc	cat	cgc	aag	341
Arg	Met	Lys	Glu	Tyr	Gly	Glu	Gln	Ile	Asp	Pro	Ser	Thr	His	Arg	Lys	
		70					75					80				
aac	tac	gta	cgt	gta	gtg	ggc	cgg	aat	gga	gaa	tcc	agt	gaa	ctg	gac	389
Asn	Tyr	Val	Arg	Val	Val	Gly	Arg	Asn	Gly	Glu	Ser	Ser	Glu	Leu	Asp	
	85					90				95						
cta	caa	ggc	atc	cga	atc	gac	tca	gat	att	agc	ggc	acc	ctc	aag	ttt	437
Leu	Gln	Gly	Ile	Arg	Ile	Asp	Ser	Asp	Ile	Ser	Gly	Thr	Leu	Lys	Phe	
	100				105				110					115		
gcg	tgt	ggg	agc	att	gtg	gag	gaa	tac	gag	gat	gaa	ctc	att	gaa	ttc	485
Ala	Cys	Gly	Ser	Ile	Val	Glu	Glu	Tyr	Glu	Asp	Glu	Leu	Ile	Glu	Phe	
				120					125					130		

ttt tcc cga gag gct gac aat gtt aaa gac aaa ctt tgc agt aag cga	533
Phe Ser Arg Glu Ala Asp Asn Val Lys Asp Lys Leu Cys Ser Lys Arg	
135 140 145	
aca gat ctt tgt gac cat gcc ctg cac ata tcg cat gat gag cta	578
Thr Asp Leu Cys Asp His Ala Leu His Ile Ser His Asp Glu Leu	
150 155 160	
tgaaccactg gagcagccca cactggcttg atggatcacc cccaggagg gaaaatggtg	638
gcaatgcctt ttatatatta tgtttttact gaaattaact gaaaaaatat gaaacaaaa	698
gtacaaaaaa aaaaaa	714

<210> 159
 <211> 596
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 33..107
 <223> Von Heijne matrix
 score 5
 seq MFAASLLAMCAGA/EV

<221> polyA_signal
 <222> 546..551

<221> polyA_site
 <222> 584..596

<400> 159	
cacagttcct ctcctcctag agcctgccga cc atg ccc gcg ggc gtg ccc atg	53
Met Pro Ala Gly Val Pro Met	
-25 -20	
tcc acc tac ctg aaa atg ttc gca gcc agt ctc ctg gcc atg tgc gca	101
Ser Thr Tyr Leu Lys Met Phe Ala Ala Ser Leu Leu Ala Met Cys Ala	
-15 -10 -5	
ggg gca gaa gtg gtg cac agg tac tac cga ccg gac ctg aca ata cct	149
Gly Ala Glu Val Val His Arg Tyr Tyr Arg Pro Asp Leu Thr Ile Pro	
1 5 10	
gaa att cca cca aag cgt gga gaa ctc aaa acg gag ctt ttg gga ctg	197
Glu Ile Pro Pro Lys Arg Gly Glu Leu Lys Thr Glu Leu Leu Gly Leu	
15 20 25 30	
aaa gaa aga aaa cac aaa cct caa gtt tct caa cag gag gaa ctt aaa	245
Lys Glu Arg Lys His Lys Pro Gln Val Ser Gln Gln Glu Glu Leu Lys	
35 40 45	
taactatgcc aagaattctg tgaataatat aagtcttaaa tatgtatttc ttaatttatt	305
gcatcaaact acttgctcctt aagcacttag tctaagtcta actgcaagag gaggtgctca	365
gtggatgttt agccgatacg ttgaaattta attacggttt gattgatatt tcttgaaaac	425
tgccaaagca catatcatca aaccatttca tgaatatggt ttggaagatg tttagtcttg	485
aatataacgc gaaatagaat atttgtaagt ctactatatg ggttgtcttt atttcatata	545
aattaagaaa ttatttaaaa ctatgaacta gtttcattaa aaaaaaaga a	596

<210> 160
 <211> 403
 <212> DNA
 <213> Homo sapiens

<220>
 <221> polyA_signal
 <222> 375..380

<221> polyA_site
 <222> 390..403

<400> 160
 tgaagagaat ggctgttgca gtcggcgctca gagcagctcc agtgccgggg attcggacgg 60
 agagcgcgag gactcggcgg ctgagcgcg cgcacagcag ctagaggcgc tgctcaacaa 120
 gact atg cgc att cgc atg aca gat gga cgg aca ctg gtc ggc tgc ttt 169
 Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe
 1 5 10 15
 ctc tgc act gac cgt gac tgc aat gtc atc ctg ggc tcg gcg cag gag 217
 Leu Cys Thr Asp Arg Asp Cys Asn Val Ile Leu Gly Ser Ala Gln Glu
 20 25 30
 ttc ctc aag ccg tcg gat tcc ttc tct gcc ggg gag ccc cgt gtg ctg 265
 Phe Leu Lys Pro Ser Asp Ser Phe Ser Ala Gly Glu Pro Arg Val Leu
 35 40 45
 ggc ctg gcc atg gta ccc gga cac cac atc gtt tcc att gag gtg cag 313
 Gly Leu Ala Met Val Pro Gly His His Ile Val Ser Ile Glu Val Gln
 50 55 60
 agg gag agt ctg acc ggg cct ccg tat ctc tgaccacgat ggcgcttacc 363
 Arg Glu Ser Leu Thr Gly Pro Pro Tyr Leu
 65 70
 tttcagactt cattaaactt atgaccaaaa aaaaaaaaaa 403

<210> 161
 <211> 727
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 126..575
 <223> Von Heijne matrix
 score 8.60000038146973
 seq LELLTSCSPPASA/SQ

<221> polyA_signal
 <222> 670..675

<221> polyA_site
 <222> 721..727

<400> 161
 ctgagaactg tgctgggaag gatggtaggg cgactggggc tcacctccgc accgttgtag 60
 gacccggggg aggggttttga gcccgtagga gctgccccac gcggcctcgt cctgccaacg 120
 gtcgg atg gcg gag acg aag gac aca gcg cag atg ttg gtg acc ttc aag 170
 Met Ala Glu Thr Lys Asp Thr Ala Gln Met Leu Val Thr Phe Lys
 -150 -145 -140
 gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg 218
 Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
 -135 -130 -125 -120
 gcc cag agg acc ctg tac cga gag ggc atc ggg ttc ccn aaa cca gag 266
 Ala Gln Arg Thr Leu Tyr Arg Glu Gly Ile Gly Phe Pro Lys Pro Glu
 -115 -110 -105

ttg gtc cac ctg cta gag cat ggg cag gag ctg tgg ata gtg aag aga	314
Leu Val His Leu Leu Glu His Gly Gln Glu Leu Trp Ile Val Lys Arg	
-100 -95 -90	
ggc ctc tca cat gct acc tgt gca gag ttt cac tct tgt tgc cca ggc	362
Gly Leu Ser His Ala Thr Cys Ala Glu Phe His Ser Cys Cys Pro Gly	
-85 -80 -75	
tgg agt gca gtg gnn cgc cat ctc agc tca ctg caa ctt ctg cct ccc	410
Trp Ser Ala Val Xaa Arg His Leu Ser Ser Leu Gln Leu Leu Pro Pro	
-70 -65 -60	
gag ttc aag gga ttc tcc tgc ctc agc ctc ccg agt agc tgg gat tac	458
Glu Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr	
-55 -50 -45 -40	
agg cgc cca cca cca tgc ccg gct ggt ttt ttt gta ttt tta gta gag	506
Arg Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val Glu	
-35 -30 -25	
acg ggg ctt cac cat gtt ggc cag gct ggt ctt gaa ctc ttg acc tca	554
Thr Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser	
-20 -15 -10	
tgt agt cca ccc gcc tct gcc tcc caa agt gct gcg att aca ggc gtg	602
Cys Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val	
-5 1 5	
agc cac cgt gcc cgg cag aga aaa act gct taagggtgaa aagagaaatt	652
Ser His Arg Ala Arg Gln Arg Lys Thr Ala	
10 15	
taagaaattg ctgacggaat aaaaacataa tagaactaca acaccgaagg aaatgaaaga	712
agcaaaaaaaaa aaaaa	727

<210> 162
 <211> 944
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 90..155
 <223> Von Heijne matrix
 score 5.90000009536743
 seq IILGCLALFLLLQ/RK

<221> polyA_signal
 <222> 913..918

<221> polyA_site
 <222> 932..944

<400> 162	
gaatcagggtt ccgtagccca cagaaaagaa gcaaggggacg gcaggactgt ttcacacttt	60
tctgcttctg gaagggtgctg gacaaaaaac atg gaa cta att tcc cca aca gtg	113
Met Glu Leu Ile Ser Pro Thr Val	
-20 -15	
att ata atc ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag	161
Ile Ile Ile Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys	
-10 -5 1	
aat ttg cgt aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga	209
Asn Leu Arg Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly	
5 10 15	
gtt gga ttt gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca	257

tgacgccatc aaggatgtct tggttctctg ttccttcttc ttggttcagg cttctgattg	470
tcctcaggct ggctcctcat agggatgctg ggtgctgcag ccttgactgg ggcagcaggc	530
ccccatgttc aatccatcct cccaccttgg aataaatgct ttctttttcac aatgagaaaa	590
aaaaaaaa	598

<210> 164
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 85..150
 <223> Von Heijne matrix
 score 5.90000009536743
 seq IILGCLALFLLLQ/RK

<221> polyA_site
 <222> 349..360

<400> 164	
caggttccgt agccacagaa aagaagcaag ggacggcagg actgtttcac acttttctgc	60
ttcttggaagg tgctggacaa aaac atg gaa cta att tcc cca aca gtg att	111
Met Glu Leu Ile Ser Pro Thr Val Ile	
-20 -15	
ata atc ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat	159
Ile Ile Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn	
-10 -5 1	
ttg cgt aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt	207
Leu Arg Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val	
5 10 15	
gga ttt gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga	255
Gly Phe Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg	
20 25 30 35	
atc aag tat gga cca ata ttt aca gtc ttt gct atg gga aac cga atg	303
Ile Lys Tyr Gly Pro Ile Phe Thr Val Phe Ala Met Gly Asn Arg Met	
40 45 50	
acc ttt gtt act gaa gaa gaa gga att aat gtg ttt cta aaa tcc	348
Thr Phe Val Thr Glu Glu Glu Gly Ile Asn Val Phe Leu Lys Ser	
55 60 65	
aaaaaaaaaa aa	360

<210> 165
 <211> 490
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 77..124
 <223> Von Heijne matrix
 score 4.80000019073486
 seq SLFIYIFLTCSNT/SP

<221> polyA_signal
 <222> 461..466

<221> polyA_site

<222> 477..490

<400> 165

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atgagcttcc agccccaaga gtggaggctg ccacatccca acatagtatc tattgaaaag      60
gaagcagtgt gtatct atg att ata tct ctg ttc atc tat ata ttt ttg aca      112
                Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr
                -15          -10          -5
tgt agc aac acc tct cca tct tat caa gga act caa ctc ggt ctg ggt      160
Cys Ser Asn Thr Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly
                1          5          10
ctc ccc agt gcc cag tgg tgg cct ttg aca ggt agg agg atg cag tgc      208
Leu Pro Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys
                15          20          25
tgc agg cta ttt tgt ttt ttg tta caa aac tgt ctt ttc cct ttt ccc      256
Cys Arg Leu Phe Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro
                30          35          40
ctc cac ctg att cag cat gat ccc tgt gag ctg gtt ctc aca atc tcc      304
Leu His Leu Ile Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser
                45          50          55          60
tgg gac tgg gct gag gca ggg gct tcg ctc tat tct ccc taaccatact      353
Trp Asp Trp Ala Glu Ala Gly Ala Ser Leu Tyr Ser Pro
                65          70
gtcttccttt ccccttgcc acttagcagt tatcccccca gctatgcctt ctccctccct      413
cccttgccct ggcatatatt gtgccttatt tatgctgcaa atataacatt aaactatcaa      473
gtgaaaaaaaa aaaaaaa      490
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<210> 166

<211> 488

<212> DNA

<213> Homo sapiens

<220>

<221> polyA_signal

<222> 458..463

<221> polyA_site

<222> 475..488

<400> 166

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ccgcttccga aaagagacag acaatgcagc catcata atg aag gtg gac aaa gac      55
                Met Lys Val Asp Lys Asp
                1          5
cgg cag atg gtg gtg ctg gag gaa gaa ttt cgg aac att tcc cca gag      103
Arg Gln Met Val Val Leu Glu Glu Phe Arg Asn Ile Ser Pro Glu
                10          15          20
gag ctc aaa atg gag ttg ccg gag aga cag ccc agg ttc gtg gtt tac      151
Glu Leu Lys Met Glu Leu Pro Glu Arg Gln Pro Arg Phe Val Val Tyr
                25          30          35
agc tac aag tac gtg cgt gac gat ggc cga gtg tcc tac cct ttg tgt      199
Ser Tyr Lys Tyr Val Arg Asp Asp Gly Arg Val Ser Tyr Pro Leu Cys
                40          45          50
ttc atc ttc tcc agc cct gtg ggc tgc aag ccg gaa caa cag atg atg      247
Phe Ile Phe Ser Ser Pro Val Gly Cys Lys Pro Glu Gln Gln Met Met
                55          60          65          70
tat gca ggg agt aaa aac agg ctg gtg cag aca gca gag ctc aca aag      295
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Tyr Ala Gly Ser Lys Asn Arg Leu Val Gln Thr Ala Glu Leu Thr Lys	
75 80 85	
gtg ttc gaa atc cgc acc act gat gac ctc act gag gcc tgg ctc caa	343
Val Phe Glu Ile Arg Thr Thr Asp Asp Leu Thr Glu Ala Trp Leu Gln	
90 95 100	
gaa aag ttg tct ttc ttt cgt tgatctctgg gctggggact gaattcctga	394
Glu Lys Leu Ser Phe Phe Arg	
105	
tgtctgagtc ctcaagggtga ctgggggactt ggaaccccta ggacctgaac aaccaagact	454
ttaaataaat tttaaaatgc aaaaaaaaaa aaaa	488

<210> 167
 <211> 771
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 48..356
 <223> Von Heijne matrix
 score 4.90000009536743
 seq VYAFLGLTAPSGS/KE

<221> polyA_signal
 <222> 742..747

<221> polyA_site
 <222> 760..771

<400> 167	
ccacagccct tttcaggacc caaacaaccg cagccgctgt tcccagg atg gtg atc	56
Met Val Ile	
cgt gta tat att gca tct tcc tct ggc tct aca gcg att aag aag aaa	104
Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile Lys Lys Lys	
-100 -95 -90 -85	
caa caa gat gtg ctt ggt ttc cta gaa gcc aac aaa ata gga ttt gaa	152
Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile Gly Phe Glu	
-80 -75 -70	
gaa aaa gat att gca gcc aat gaa gag aat cgg aag tgg atg aga gaa	200
Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp Met Arg Glu	
-65 -60 -55	
aat gta cct gag aat agt cga cca gcc aca ggt aac ccc ctg cca cct	248
Asn Val Pro Glu Asn Ser Arg Pro Ala Thr Gly Asn Pro Leu Pro Pro	
-50 -45 -40	
cag att ttc aat gaa agc cag tat cgc ggg gac tat gat gcc ttc ttt	296
Gln Ile Phe Asn Glu Ser Gln Tyr Arg Gly Asp Tyr Asp Ala Phe Phe	
-35 -30 -25	
gaa gcc aga gaa aat aat gca gtg tat gcc ttc tta ggc ttg aca gcc	344
Glu Ala Arg Glu Asn Asn Ala Val Tyr Ala Phe Leu Gly Leu Thr Ala	
-20 -15 -10 -5	
cca tct ggt tca aag gaa gca gaa gtg caa gca aag cag caa gca	389
Pro Ser Gly Ser Lys Glu Ala Glu Val Gln Ala Lys Gln Gln Ala	
1 5 10	
tgaaccttga gcaactgtgct ttaagcatcc tgaaaaatga gtctccattg cttttataaa	449
atagcagaat tagcttttgc tcaaaagaaa taggcttaat gttgaaataa tagattagtt	509
gggttttcac atgcaaacac tcaaaatgaa tacaaaatta aaatttgaac attatggtga	569
ttatggtgag gagaatggga tattaacata aaattatatt aataagtaga tatcgtagaa	629

atagtgttgt tacctgccaa gccatcctgt atacaccaat gattttacaa agaaaacacc	689
cttccctcct tctgccatta ctatggcaac ctaagtgtat ctgcagctct acattaaaaa	749
ggagaaagag aaaaaaaaaa aa	771

<210> 168
 <211> 959
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 69..359
 <223> Von Heijne matrix
 score 4
 seq RLPLVVSFIASSS/AN

<221> polyA_signal
 <222> 927..932

<221> polyA_site
 <222> 947..959

<400> 168	
cggagagaaac caggcagccc agaaacccca ggcgtggaga ttgatcctgc gagagaaggg	60
ggttcatc atg gcg gat gac cta aag cga ttc ttg tat aaa aag tta cca	110
Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro	
-95 -90 -85	
agt gtt gaa ggg ctc cat gcc att gtt gtg tca gat aga gat gga gta	158
Ser Val Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val	
-80 -75 -70	
cct gtt att aaa gtg gca aat gac aat gct cca gag cat gct ttg cga	206
Pro Val Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg	
-65 -60 -55	
cct ggt ttc tta tcc act ttt gcc ctt gca aca gac caa gga agc aaa	254
Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys	
-50 -45 -40	
ctt gga ctt tcc aaa aat aaa agt atc atc tgt tac tat aac acc tac	302
Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr	
-35 -30 -25 -20	
cag gtg gtt caa ttt aat cgt tta cct ttg gtg gtg agt ttc ata gcc	350
Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala	
-15 -10 -5	
agc agc agt gcc aat aca gga cta att gtc agc cta gaa aag gaa ctt	398
Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu	
1 5 10	
gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa gtt tct	440
Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser	
15 20 25	
taatctgaca gtggtttcag tgtgtacctt atcttcatta taacaacaca atatcaatcc	500
agcaatcttt agactacaat aatactttta tccatgtgct caagaaaggg cccctttttc	560
caacttatac taaagagcta gcatatagat gtaatttata gatagatcag ttgctatatt	620
ttctggtgta gggcttttct tatttagtga gatctagga taccacagaa atggttcagt	680
ctatcacagc tcccatggag ttagtctggg caccagatat ggatgagaga ttctattcag	740
tggatcagaa tcaaactggt acattgatcc acttgagccg ttaagtgtg ccaattgtac	800
aatatgccca ggcttgcaaga ataaagccaa ctttttattg tgaataataa taaggacata	860
tttttcttca gattatgttt tattttctttg cattgagtga ggaacataaa atggcttggt	920
aaaagtaata aaatcagtac aatcactaaa aaaaaaaaaa	959

<210> 169
 <211> 464
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 33..98
 <223> Von Heijne matrix
 score 9.80000019073486
 seq LVVFCLALQLVPG/SP

<221> polyA_signal
 <222> 437..442

<221> polyA_site
 <222> 455..464

<400> 169
 gccagaactt actcaccat cccactgaca cc atg aag cct gtg ctg cct ctc 53
 Met Lys Pro Val Leu Pro Leu
 -20
 cag ttc ctg gtg gtg ttc tgc cta gca ctg cag ctg gtg cct ggg agt 101
 Gln Phe Leu Val Val Phe Cys Leu Ala Leu Gln Leu Val Pro Gly Ser
 -15 -10 -5 1
 ccc aag cag cgt gtt ctg aag tat atc ttg gaa cct cca ccc tgc ata 149
 Pro Lys Gln Arg Val Leu Lys Tyr Ile Leu Glu Pro Pro Pro Cys Ile
 5 10 15
 tca gca cct gaa aac tgt act cac ctg tgt aca atg cag gaa gat tgc 197
 Ser Ala Pro Glu Asn Cys Thr His Leu Cys Thr Met Gln Glu Asp Cys
 20 25 30
 gag aaa gga ttt cag tgc tgt tcc tcc ttc tgt ggg ata gtc tgt tca 245
 Glu Lys Gly Phe Gln Cys Cys Ser Ser Phe Cys Gly Ile Val Cys Ser
 35 40 45
 tca gaa aca ttt caa aag cgc aac aga atc aaa cac aag ggc tca gaa 293
 Ser Glu Thr Phe Gln Lys Arg Asn Arg Ile Lys His Lys Gly Ser Glu
 50 55 60 65
 gtc atc atg cct gcc aac tgaggcatat ttcttagatc attttgcctc 341
 Val Ile Met Pro Ala Asn
 70
 tacgatgttt tttcttggtc cacctttagg aaggtattga gaagcaagaa actggaggcc 401
 caatatctaa cctgcaaatac gtttttgagt ttggcaataa aggctaatac accaaaaaaa 461
 aaa 464

<210> 170
 <211> 799
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 110..235
 <223> Von Heijne matrix
 score 5.19999980926514
 seq LLFDLVCHEFCQS/DD

<221> polyA_signal
 <222> 764..769

<221> polyA_site
 <222> 787..799

<400> 170

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ccaaccccag gaagagtctg aagagcagcc agtgtttcgg cttgtgccct gtataacttga      60
agctgcca aaa caagtacgtt ctgaaaatcc agaatggcct gatgtttac atg cac att      118
                                     Met His Ile
                                     -40
tta caa ctg ctt act aca gtg gat gat gga att caa gca att gta cat      166
Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His
                                     -35                                     -25
tgt cct gac act gga aaa gac att tgg aat cta ctt ttt gac ctg gtc      214
Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val
                                     -20                                     -15                                     -10
tgc cat gaa ttc tgc cag tct gat gat cca ccc atc att ctt caa gaa      262
Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile Leu Gln Glu
                                     -5                                     1                                     5
cag aaa aca gtg cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat      310
Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr
10                                     15                                     20                                     25
gcc tca cag act gag caa gag tat cta aag ata gaa aaa gta gat ctt      358
Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val Asp Leu
                                     30                                     35                                     40
cct cta att gac agc ctc att cgg gtc tta caa aat atg gaa cag tgt      406
Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met Glu Gln Cys
                                     45                                     50                                     55
cag aaa aaa cca gag aac tcg gca gag tct aac aca gag gaa act aaa      454
Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu Glu Thr Lys
60                                     65                                     70
agg act gat tta acc caa gat gat ttc cac ttg aaa atc tta aag gat      502
Arg Thr Asp Leu Thr Gln Asp Asp Phe His Leu Lys Ile Leu Lys Asp
75                                     80                                     85
att tta tgt gaa ttt ctt tct aat att ttt cag gca tta aca aag gag      550
Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu Thr Lys Glu
90                                     95                                     100                                     105
acg gtg gct cag gga gta aag gaa ggc cag ttg agc aaa cag aag tgt      598
Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys Gln Lys Cys
                                     110                                     115                                     120
tcc tct gca ttt caa aac ctt ctt cct ttc tat agc cct gtg gtg gaa      646
Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro Val Val Glu
125                                     130                                     135
gat ttt att aaa atc cta cgt gaa gtt gat aag gcg ctt gct gat gac      694
Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu Ala Asp Asp
140                                     145                                     150
ttg gaa aaa aac ttc cca agt ttg aag gtt cag act taaaacctga      740
Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr
155                                     160                                     165
attggaatta cttctgtaca agaaataaac tttatattttc tcactgaaaa aaaaaaaaaa      799

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<210> 171
 <211> 320
 <212> DNA
 <213> Homo sapiens

<220>

<221> polyA_site

<222> 308..320

<400> 171

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tcatcatcca gagcagccag tgtccgggag gcagaag atg ccc cac tcc aag cct      55
                               Met Pro His Ser Lys Pro
                               1       5
ctg gac tgg ggg ctc tct tca gtg gct gaa tgt cca gca gag cta ttt      103
Leu Asp Trp Gly Leu Ser Ser Val Ala Glu Cys Pro Ala Glu Leu Phe
          10       15       20
cct tcc aca ggg ggc ctt gca ggg aag ggt cca gga ctt gac atc tta      151
Pro Ser Thr Gly Gly Leu Ala Gly Lys Gly Pro Gly Leu Asp Ile Leu
          25       30       35
aga tgc gtc ttg tcc cct tgg gcc agt cat ttc ccc tct ctg agc ctc      199
Arg Cys Val Leu Ser Pro Trp Ala Ser His Phe Pro Ser Leu Ser Leu
          40       45       50
ggg gtc ttc aac ctg tgaaatggga tcataatcac tgccttacct ccctcacggt      254
Gly Val Phe Asn Leu
55
tggtgtgagg actgagtgtg tggaagtttt tcataaactt tggatgctag tgtaaaaaaa      314
aaaaaa                                     320
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<210> 172

<211> 331

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 129..209

<223> Von Heijne matrix
score 4.90000009536743
seq CLLSYIALGAIHA/KI

<221> polyA_site

<222> 318..331

<400> 172

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atggaaacca gatggggcaa cgggggtggtt ctagtgcaga ctgtagctgc agctcctctc      60
cacctctagc ctgctcattt ccagctcaga aattctacta atggcgtttt ttcttcctga      120
aaaaggaa atg aac agg gtc cct gct gat tct cca aat atg tgt cta atc      170
          Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile
          -25       -20       -15
tgt tta ctg agt tac ata gca ctt gga gcc atc cat gca aaa atc tgt      218
Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys
          -10       -5       1
agg aga gca ttc cag gaa gag gga aga gca aat gca aag acg ggc gtg      266
Arg Arg Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val
          5       10       15
aga gct tgg tgc ata cag cca tgg gcc aaa taaagtttcc ttggaatagc      316
Arg Ala Trp Cys Ile Gln Pro Trp Ala Lys
20       25
caaaaaaaaa aaaaaa                                     331
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<210> 173
 <211> 1075
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 78..359
 <223> Von Heijne matrix
 score 4.19999980926514
 seq IILTAVYFALSIS/LH

<221> polyA_signal
 <222> 1042..1047

<221> polyA_site
 <222> 1063..1075

<400> 173
 gtggtaggga gcagccagga gcggttttct gggaactgtg ggatgtgccc ttggggggccc 60
 gagaaaacag aaggaag atg ctc cag acc agt aac tac agc ctg gtg ctc 110
 Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu
 -90 -85
 tct ctg cag ttc ctg ctg ctg tcc tat gac ctc ttt gtc aat tcc ttc 158
 Ser Leu Gln Phe Leu Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe
 -80 -75 -70
 tca gaa ctg ctc caa aag act cct gtc atc cag ctt gtg ctc ttc atc 206
 Ser Glu Leu Leu Gln Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile
 -65 -60 -55
 atc cag gat att gca gtc ctc ttc aac atc atc atc att ttc ctc atg 254
 Ile Gln Asp Ile Ala Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met
 -50 -45 -40
 ttc ttc aac acc ttc gtc ttc cag gct ggc ctg gtc aac ctc cta ttc 302
 Phe Phe Asn Thr Phe Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe
 -35 -30 -25 -20
 cat aag ttc aaa ggg acc atc atc ctg aca gct gtg tac ttt gcc ctc 350
 His Lys Phe Lys Gly Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu
 -15 -10 -5
 agc atc tcc ctt cat gtc tgg gtc atg aac tta cgc tgg aaa aac tcc 398
 Ser Ile Ser Leu His Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser
 1 5 10
 aac agc ttc ata tgg aca gat gga ctt caa atg ctg ttt gta ttc cag 446
 Asn Ser Phe Ile Trp Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln
 15 20 25
 aga cta gca gca gtg ttg tac tgc tac ttc tat aaa cgg aca gcc gta 494
 Arg Leu Ala Ala Val Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val
 30 35 40 45
 aga cta ggc gat cct cac ttc tac cag gac tct ttg tgg ctg cgc aag 542
 Arg Leu Gly Asp Pro His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys
 50 55 60
 gag ttc atg caa gtt cga agg tgacctcttg tcacactgat ggatactttt 593
 Glu Phe Met Gln Val Arg Arg
 65
 ccttcctgat agaagccaca tttgctgctt tgcagggaga gttggcccta tgcattgggca 653
 aacagctgga ctttccaagg aagggttcaga ctactgtgtg tcagcattca agaaggaaga 713
 tccccctct tgcacaatta gagtgtcccc atcggtctcc agtgcggcac cccttccttg 773
 ccttctacct ctgttccacc cccttccttc ctctcctctc tgtaccattc attctccctg 833
 accggccttt cttgccgagg gttctgtggc tcttaccctt gtgaagcttt tccttttagcc 893

tgggacagaa	ggacctcccg	gccccaaaag	gatctcccag	tgaccaaagg	atgcgaagag	953
tgatagttac	gtgctcctga	ctgatcacac	cgagacatt	tagattttta	tacccaaggc	1013
actttaaaaa	aatgttttat	aaatagagaa	taaattgaat	tcttgttcca	aaaaaaaaaa	1073
aa						1075

<210> 174
 <211> 632
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 62..265
 <223> Von Heijne matrix
 score 4.59999990463257
 seq LPFSLVSMMLVTQG/LV

<221> polyA_signal
 <222> 602..607

<221> polyA_site
 <222> 621..632

<400> 174	
cactgggtca	aggagtaagc agaggataaaa caactggaag gagagcaagc acaaagtcac 60
c atg gct tca gcg tct gct cgt gga aac caa gat aaa gat gcc cat ttt	109
Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe	
-65 -60 -55	
cca cca cca agc aag cag agc ctg ttg ttt tgt cca aaa tca aaa ctg	157
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu	
-50 -45 -40	
cac atc cac aga gca gag atc tca aag att atg cga gaa tgt cag gaa	205
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu	
-35 -30 -25	
gaa agt ttc tgg aag aga gct ctg cct ttt tct ctt gta agc atg ctt	253
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu	
-20 -15 -10 -5	
gtc acc cag gga cta gtc tac caa ggt tat ttg gca gct aat tct aga	301
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg	
1 5 10	
ttt gga tca ttg ccc aaa gtt gca ctt gct ggt ctc ttg gga ttt ggc	349
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly	
15 20 25	
ctt gga aag gta tca tac ata gga gta tgc cag agt aaa ttc cat ttt	397
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe	
30 35 40	
ttt gaa gat cag ctc cgt ggg gct ggt ttt ggt cca cag cat aac agg	445
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His Asn Arg	
45 50 55 60	
cac tgc ctc ctt acc tgt gag gaa tgc aaa ata aag cat gga tta agt	493
His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly Leu Ser	
65 70 75	
gag aag gga gac tct cag cct tca gct tcc taaattctgt gtctgtgact	543
Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser	
80 85	
ttcgaagttt tttaaacctc tgaatttgta cacatttaaa atttcaagtg tactttaaaa	603
taaaatactt ctaatgtaaa aaaaaaaaaa	632

<210> 175
 <211> 430
 <212> DNA
 <213> Homo sapiens

<220>
 <221> polyA_signal
 <222> 402..407

<221> polyA_site
 <222> 419..430

<400> 175

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gtattgggaa agtgatttgt gaa atg aaa gta gaa gaa gag cat acc aat gca      53
                        Met Lys Val Glu Glu Glu His Thr Asn Ala
                        1         5         10
ata ggc act ctc cac ggc ggt ttg aca gcc acg tta gta gat aac ata      101
Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile
                        15         20         25
tca aca atg gct ctg cta tgc acg gaa agg gga gca ccc gga gtc agt      149
Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser
                        30         35         40
gtc gat atg aac ata acg tac atg tca cct gca aaa tta gga gag gat      197
Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp
                        45         50         55
ata gtg att aca gca cat gtt ctg aag caa gga aaa aca ctt gca ttt      245
Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe
                        60         65         70
acc tct gtg ggt ctg acc aac aag gcc aca gga aaa tta ata gca caa      293
Thr Ser Val Gly Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln
                        75         80         85         90
gga aga cac aca aaa cac ctg gga aac tgagagaaca gcagaatgac      340
Gly Arg His Thr Lys His Leu Gly Asn
                        95
ctaaagaaac ccaacaatga atatcaagta tagatttgac tcaaacaatt gtaatttttg      400
aaataaacta gcaaaaccaa aaaaaaaaaa      430

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<210> 176
 <211> 185
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 42..113
 <223> Von Heijne matrix
 score 3.70000004768372
 seq ILFNLLIFLCGFT/NY

<221> polyA_site
 <222> 172..185

<400> 176

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ctttcagaac tcaactgccaa gagccctgaa caggagccac c atg cag tgc ttc agc      56
                        Met Gln Cys Phe Ser

```

-20

ttc att aag acc atg atg atc ctc ttc aat ttg ctc atc ttt ctg tgt	104
Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe Leu Cys	
-15 -10 -5	
ggc ttc acc aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg	152
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met	
1 5 10	
cat aaa cct gtt aca atg taaaaaaaa aaaaa	185
His Lys Pro Val Thr Met	
15	

<210> 177
 <211> 585
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 108..170
 <223> Von Heijne matrix
 score 5.5
 seq SFLPSALVIWTS/AF

<221> polyA_signal
 <222> 550..555

<221> polyA_site
 <222> 574..585

<400> 177

cacgttcctg ttgagtacac gttcctgttg atttacaaaa ggtgcaggta tgagcaggtc	60
tgaagactaa cattttgtga agttgtaaaa cagaaaacct gttagaa atg tgg tgg	116
Met Trp Trp	
-20	
ttt cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca	164
Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr	
-15 -10 -5	
ttct gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat	212
Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His	
1 5 10	
ata gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca	260
Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro	
15 20 25 30	
gaa aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtc tta tgt	308
Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys	
35 40 45	
caa aaa tagaaatcag gaagataatt caacttaaag aagttcattt catgaccaa	364
Gln Lys	
ctcttcagaa acatgtcttt acaagcatat ctcttgatt gctttctaca ctgttgaatt	424
gtctggcaat atttctgcag tggaaaattt gatttagcta gttcttgact gataaatatg	484
gtaagggtggg cttttccccc tgtgtaattg gctactatgt cttactgagc caagttgtaa	544
tttgaaataa aatgatatga gactgacaca aaaaaaaaaa a	585

<210> 178
 <211> 613
 <212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 118..171

<223> Von Heijne matrix

score 5.90000009536743

seq ALALLWSLPASDL/GR

<221> polyA_signal

<222> 583..588

<221> polyA_site

<222> 602..613

<400> 178

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ggggtgggtg gactagaagc atttgggagt agtggccagg ggccctggac gctagccacg      60
gagctgccgc acagagcctg gtgtccacaa gcttccaggt tggggttgga gcctggg      117
atg agc ccc ggc agc gcc ttg gcc ctt ctg tgg tcc ctg cca gcc tct      165
Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser
          -15                -10                -5
gac ctg ggc cgg tca gtc att gct gga ctc tgg cca cac act ggc gtt      213
Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val
          1                5                10
ctc atc cac ttg gaa aca agc cag tct ttt ctg caa ggt cag ttg acc      261
Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr
          15                20                25                30
aag agc ata ttt ccc ctc tgt tgt aca tcg ttg ttt tgt gtt tgt gtt      309
Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val
          35                40                45
gta aca gtg ggt gga ggg agg gtg ggg tct aca ttt gtt gca      351
Val Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala
          50                55                60
tgagtcgatg ggtcagaact ttagtatacg catgcgtcct ctgagtgaca gggcattttg      411
tcgaaaataa gcaccttggg aactaaaccc ctctaatagc tataaaggct ttagttctgt      471
attgattaag ttactgtaaa agcttgggtt tatttttgta ggacttaatg gctaagaatt      531
agaacatagc aagggggctc ctctgttgga gtaatgtaaa ttgtaattat aaataaacat      591
gcaaaccctt aaaaaaaaaa aa      613
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<210> 179

<211> 427

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 128..268

<223> Von Heijne matrix

score 5.5

seq SALLFFARPCVFC/FK

<221> polyA_signal

<222> 410..415

<221> polyA_site

<222> 424..427

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<400> 179
agcttgatt tacactgggc aacgtggttg gaatgtatct ggctcagaac tatgatatac      60
caaacctggc taaaaaactt gaagaaatta aaaaggactt ggatgccaaag aagaaacccc    120
ctagtgc atg aga ctg cct cca gca ctg cct tca gga tat act gat tct      169
      Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser
            -45                      -40                      -35
act gct ctt gag ggc ctc gtt tac tat ctg aac caa aag ctt ttg ttt      217
Thr Ala Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe
            -30                      -25                      -20
tcg tct cca gcc tca gca ctt ctc ttc ttt gct aga ccc tgt gtt ttt      265
Ser Ser Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe
            -15                      -10                      -5
tgc ttt aaa gca agc aaa atg ggg ccc caa ttt gag aac tac cca aca      313
Cys Phe Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr
      1              5              10              15
ttt cca aca tac tca cct ctt ccc ata atc cct ttc caa ctg cat ggg      361
Phe Pro Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly
            20              25              30
agg ttc taagactgga attatggtgc tagattagta aacatgactt ttaatgaaaa      417
Arg Phe
aaaaacaaaa      427

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<210> 180
<211> 905
<212> DNA
<213> Homo sapiens

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<220>
<221> sig_peptide
<222> 149..457
<223> Von Heijne matrix
      score 4.90000009536743
      seq FLQAQTTLRNVLG/TQ

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<221> polyA_site
<222> 893..912

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<400> 180
gctgcctggt cttcacactt agctccaaac ccatgaaaaa ttgccaagta taaaagcttc      60
tcaagaatga gatggattct aggggtgtctt cacctgagaa gcaagataaa gagaatttcg    120
tggtgtcaa caataaacgg cttggtgt atg tgg ctg gat cct gtt ttc cct      172
      Met Trp Leu Asp Pro Val Phe Pro
            -100
ctc ttt cct gtt ggt gat cat tac ctt ccc cat ctc cat atg gat gtg      220
Leu Phe Pro Val Gly Asp His Tyr Leu Pro His Leu His Met Asp Val
      -95              -90              -85              -80
ctt gaa ggt ttg atc ctg gtc ctg cca tgc ata gat gtg ttt gtc aaa      268
Leu Glu Gly Leu Ile Leu Val Leu Pro Cys Ile Asp Val Phe Val Lys
            -75              -70              -65
gtt gac ctc cga aca gtt act tgc aac att cct cca caa gag atc ctc      316
Val Asp Leu Arg Thr Val Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu
            -60              -55              -50
acc aga gac tcc gta act act cag gta gat gga gtt gtc tat tac aga      364
Thr Arg Asp Ser Val Thr Thr Gln Val Asp Gly Val Val Tyr Tyr Arg
            -45              -40              -35
atc tat agt gct gtc tca gca gtg gct aat gtc aac gat gtc cat caa      412
Ile Tyr Ser Ala Val Ser Ala Val Ala Asn Val Asn Asp Val His Gln

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-30	-25	-20	
gca aca ttt ctg ctg gct caa acc act ctg aga aat gtc tta ggg aca			460
Ala Thr Phe Leu Leu Ala Gln Thr Thr Leu Arg Asn Val Leu Gly Thr			
-15	-10	-5	1
cag acc ttg tcc cag atc tta gct gga cga gaa gag atc gcc cat agc			508
Gln Thr Leu Ser Gln Ile Leu Ala Gly Arg Glu Glu Ile Ala His Ser			
5	10	15	
atc cag act tta ctt gat gat gcc acc gaa ctg tgg ggg atc cgg gtg			556
Ile Gln Thr Leu Leu Asp Asp Ala Thr Glu Leu Trp Gly Ile Arg Val			
20	25	30	
gcc cga gtg gaa atc aaa gat gtt cgg att ccc gtg cag ttg cag aga			604
Ala Arg Val Glu Ile Lys Asp Val Arg Ile Pro Val Gln Leu Gln Arg			
35	40	45	
tcc atg gca gcc gag gct gag gcc acc cgg gaa gcg aga gcc aag gtc			652
Ser Met Ala Ala Glu Ala Glu Ala Thr Arg Glu Ala Arg Ala Lys Val			
50	55	60	65
ctt gca gct gaa gga gaa atg aat gct tcc aaa tcc ctg aag tca gcc			700
Leu Ala Ala Glu Gly Glu Met Asn Ala Ser Lys Ser Leu Lys Ser Ala			
70	75	80	
tcc atg gtg ctg gct gag tct ccc ata gct ctc cag ctg cgc tac ctg			748
Ser Met Val Leu Ala Glu Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu			
85	90	95	
cag acc ttg agc acg gta gcc acc gag aag aat tct acg att gtg ttt			796
Gln Thr Leu Ser Thr Val Ala Thr Glu Lys Asn Ser Thr Ile Val Phe			
100	105	110	
cct ctg ccc atg aat ata cta gag ggc att ggt ggc gtc agc tat gat			844
Pro Leu Pro Met Asn Ile Leu Glu Gly Ile Gly Val Ser Tyr Asp			
115	120	125	
aac cac aag aag ctt cca aat aaa gcc tgaggctctc ttgcggtagt			891
Asn His Lys Lys Leu Pro Asn Lys Ala			
130	135		
caaaaaaaaaaaaa			905

<210> 181
 <211> 307
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

<400> 181
 Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu
 -10 -5 1
 Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
 5 10 15
 Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
 20 25 30 35
 Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
 40 45 50
 Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu
 55 60 65
 Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys
 70 75 80
 Lys Thr Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg
 85 90 95

Ala	Gly	Pro	Asn	Gly	Thr	Leu	Phe	Val	Ala	Asp	Ala	Tyr	Lys	Gly	Leu
100					105					110					115
Phe	Glu	Val	Asn	Pro	Trp	Lys	Arg	Glu	Val	Lys	Leu	Leu	Leu	Ser	Ser
			120						125					130	
Glu	Thr	Pro	Ile	Glu	Gly	Lys	Asn	Met	Ser	Phe	Val	Asn	Asp	Leu	Thr
			135					140					145		
Val	Thr	Gln	Asp	Gly	Arg	Lys	Ile	Tyr	Phe	Thr	Asp	Ser	Ser	Ser	Lys
		150				155						160			
Trp	Gln	Arg	Arg	Asp	Tyr	Leu	Leu	Val	Met	Glu	Gly	Thr	Asp	Asp	
	165					170				175					
Gly	Arg	Leu	Leu	Glu	Tyr	Asp	Thr	Val	Thr	Arg	Glu	Val	Lys	Val	Leu
180					185					190					195
Leu	Asp	Gln	Leu	Arg	Phe	Pro	Asn	Gly	Val	Gln	Leu	Ser	Pro	Ala	Glu
			200						205					210	
Asp	Phe	Val	Leu	Val	Ala	Glu	Thr	Thr	Met	Ala	Arg	Ile	Arg	Arg	Val
		215						220					225		
Tyr	Val	Ser	Gly	Leu	Met	Lys	Gly	Gly	Ala	Asp	Leu	Phe	Val	Glu	Asn
		230					235					240			
Met	Pro	Gly	Phe	Pro	Asp	Asn	Ile	Arg	Pro	Ser	Ser	Ser	Gly	Gly	Tyr
	245					250				255					
Trp	Val	Gly	Met	Ser	Thr	Ile	Arg	Pro	Asn	Pro	Gly	Phe	Ser	Met	Leu
260					265					270					275
Asp	Phe	Leu	Ser	Glu	Arg	Pro	Trp	Ile	Lys	Arg	Met	Ile	Phe	Lys	Val
				280					285					290	
Lys	Lys	Lys													

<210> 182
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>

<400> 182

Met	Met	Tyr	Val	Ser	Ile	Glu	Met	Ser	Gly	Pro	Thr	Ile	Ser	His	Leu
1				5					10					15	
Phe	Asp	Tyr	Val	Val	Cys	Tyr	Ile	Tyr	Gly	Leu	Lys	Ser	Phe	Ser	Leu
			20					25					30		
Lys	Gln	Leu	Lys	Lys	Lys	Ser	Trp	Ser	Lys	Tyr	Leu	Phe	Glu	Ser	Cys
		35					40					45			
Cys	Tyr	Arg	Ser	Leu	Tyr	Val	Cys	Val	Phe	Ile					
	50					55									

<210> 183
 <211> 97
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
 <222> -28...-1

<400> 183

Met	Ser	Pro	Ala	Phe	Arg	Ala	Met	Asp	Val	Glu	Pro	Arg	Ala	Lys	Gly
			-25					-20					-15		
Val	Leu	Leu	Glu	Pro	Phe	Val	His	Gln	Val	Gly	Gly	His	Ser	Cys	Val

		-10						-5				1					
Leu	Arg	Phe	Asn	Glu	Thr	Thr	Leu	Cys	Lys	Pro	Leu	Val	Pro	Arg	Glu		
5						10				15					20		
His	Gln	Phe	Tyr	Glu	Thr	Leu	Pro	Ala	Glu	Met	Arg	Lys	Phe	Ser	Pro		
			25						30					35			
Gln	Tyr	Lys	Gly	Gln	Ser	Gln	Arg	Pro	Leu	Val	Ser	Trp	Pro	Ser	Leu		
		40					45					50					
Pro	His	Phe	Phe	Pro	Trp	Ser	Phe	Pro	Leu	Trp	Pro	Gln	Gly	Ser	Val		
		55					60					65					
Ala																	

<210> 184
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 184

Met	Leu	Gly	Thr	Thr	Gly	Leu	Gly	Thr	Gln	Gly	Pro	Ser	Gln	Gln	Ala		
		-30				-25					-20						
Leu	Gly	Phe	Phe	Ser	Phe	Met	Leu	Leu	Gly	Met	Gly	Gly	Cys	Leu	Pro		
	-15					-10				-5							
Gly	Phe	Leu	Leu	Gln	Pro	Pro	Asn	Arg	Ser	Pro	Thr	Leu	Pro	Ala	Ser		
1				5					10					15			
Thr	Phe	Ala	His														
			20														

<210> 185
 <211> 124
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -97..-1

<400> 185

Met	Ala	Asp	Asp	Leu	Lys	Arg	Phe	Leu	Tyr	Lys	Lys	Leu	Pro	Ser	Val		
		-95				-90						-85					
Glu	Gly	Leu	His	Ala	Ile	Val	Val	Ser	Asp	Arg	Asp	Gly	Val	Pro	Val		
	-80					-75					-70						
Val	Lys	Val	Ala	Asn	Asp	Asn	Ala	Pro	Glu	His	Ala	Leu	Arg	Pro	Gly		
	-65				-60					-55					-50		
Phe	Leu	Ser	Thr	Phe	Ala	Leu	Ala	Thr	Asp	Gln	Gly	Ser	Lys	Leu	Gly		
			-45					-40						-35			
Leu	Ser	Lys	Asn	Lys	Ser	Ile	Ile	Cys	Tyr	Tyr	Asn	Thr	Tyr	Gln	Val		
		-30				-25					-20						
Val	Gln	Phe	Asn	Arg	Leu	Pro	Leu	Val	Val	Ser	Phe	Ile	Ala	Ser	Ser		
	-15					-10					-5						
Ser	Ala	Asn	Thr	Gly	Leu	Ile	Val	Ser	Leu	Glu	Lys	Glu	Leu	Ala	Pro		
	1				5				10						15		
Leu	Phe	Glu	Glu	Leu	Arg	Gln	Val	Val	Glu	Val	Ser						
			20						25								

<210> 186
 <211> 230
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 186
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
 -20 -15 -10
 Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
 -5 1 5
 Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys
 10 15 20
 Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys
 25 30 35 40
 Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala
 45 50 55
 Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile
 60 65 70
 Ile Ser Val Val Gly Met Arg Cys Thr Val Phe Cys Gln Glu Ser Arg
 75 80 85
 Ala Lys Asp Arg Val Ala Val Ala Gly Gly Val Phe Phe Ile Leu Gly
 90 95 100
 Gly Leu Leu Gly Phe Ile Pro Val Ala Trp Asn Leu His Gly Ile Leu
 105 110 115 120
 Arg Asp Phe Tyr Ser Pro Leu Val Pro Asp Ser Met Lys Phe Glu Ile
 125 130 135
 Gly Glu Ala Leu Tyr Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile
 140 145 150
 Ala Gly Ile Ile Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser
 155 160 165
 Asn Tyr Tyr Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser
 170 175 180
 Pro Arg Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr
 185 190 195 200
 Ser Leu Thr Gly Tyr Val
 205

<210> 187
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 187
 Met Phe Ala Leu Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
 Gly Tyr Gly Val Pro Met Leu Leu Ile Ala Gly Gly Ser Phe Gly
 -15 -10 -5

Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
 1 5 10 15
 Asp Pro Glu Leu Glu Lys Lys Pro Lys Glu Asn Lys Ile Ser Leu Glu
 20 25 30
 Ser Glu Tyr Glu Gly Ser Ile Cys
 35 40

<210> 188
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33..-1

<400> 188
 Met Ser Gln Thr Ala Trp Leu Ser Leu Leu Ser Ser Ser Pro Phe Gly
 -30 -25 -20
 Pro Phe Ser Ala Leu Thr Phe Leu Phe Leu His Leu Pro Pro Ser Thr
 -15 -10 -5
 Ser Leu Phe Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly Pro Leu Gly
 1 5 10 15
 Leu Ile Leu Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys Cys Asp Phe
 20 25 30
 Ala Leu Ser Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe Ser Ile Met
 35 40 45
 Asp Pro Lys Arg Lys Thr Lys Cys
 50 55

<210> 189
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 189
 Met Phe Ala Pro Ala Val Thr Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
 Gly Tyr Gly Val Pro Met Leu Leu Ile Val Gly Gly Ser Phe Gly
 -15 -10 -5
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
 1 5 10 15
 Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
 20 25 30
 Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
 35 40 45
 Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
 50 55 60
 Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
 65 70

<210> 190
 <211> 267
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 190
 Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
 -20 -15 -10
 Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
 -5 1 5 10
 Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
 15 20 25
 Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
 30 35 40
 Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr Lys Gln Val His Ala
 45 50 55
 Leu Ser Pro Glu Glu Asn Val Ile Ile Lys Leu Asn Lys Ala Gly Leu
 60 65 70 75
 Val Leu Gly Ile Leu Ser Cys Leu Gly Leu Ser Ile Val Ala Asn Phe
 80 85 90
 Gln Lys Thr Thr Leu Phe Ala Ala His Val Ser Gly Ala Val Leu Thr
 95 100 105
 Phe Gly Met Gly Ser Leu Tyr Met Phe Val Gln Thr Ile Leu Ser Tyr
 110 115 120
 Gln Met Gln Pro Lys Ile His Gly Lys Gln Val Phe Trp Ile Arg Leu
 125 130 135
 Leu Leu Val Ile Trp Cys Gly Val Ser Ala Leu Ser Met Leu Thr Cys
 140 145 150 155
 Ser Ser Val Leu His Ser Gly Asn Phe Gly Thr Asp Leu Glu Gln Lys
 160 165 170
 Leu His Trp Asn Pro Glu Asp Lys Gly Tyr Ala Leu His Met Ile Thr
 175 180 185
 Thr Ala Ala Glu Trp Ser Met Ser Phe Ser Phe Phe Gly Phe Phe Leu
 190 195 200
 Thr Tyr Ile Arg Asp Phe Gln Lys Ile Ser Leu Arg Val Glu Ala Asn
 205 210 215
 Leu His Gly Leu Thr Leu Tyr Asp Thr Ala Pro Cys Pro Ile Asn Asn
 220 225 230 235
 Glu Arg Thr Arg Leu Leu Ser Arg Asp Ile Arg
 240 245

<210> 191
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>

<400> 191
 Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile
 1 5 10 15
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
 20 25 30

Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 35 40 45
 Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
 50 55 60
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 65 70 75 80
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 85 90 95
 Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr
 100 105

<210> 192
 <211> 69
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -46..-1

<400> 192

Met Ser Val Phe Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile
 -45 -40 -35
 Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys
 -30 -25 -20 -15
 Ser Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu
 -10 -5 1
 Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Leu
 5 10 15
 Lys Tyr His Trp Pro
 20

<210> 193
 <211> 251
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 193

Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro
 -25 -20 -15
 Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr
 -10 -5 1
 Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro
 5 10 15 20
 Lys Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys Val Arg Arg
 25 30 35
 Glu Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr
 40 45 50
 Glu Phe Thr Glu Gly Asn Phe Ala Ile Leu Ala Leu Gly Gly Gly Tyr
 55 60 65
 Leu His Trp Gly His Phe Glu Met Met Arg Leu Thr Ile Asn Arg Ser
 70 75 80

Met	Asp	Pro	Lys	Asn	Met	Phe	Ala	Ile	Trp	Arg	Val	Pro	Ala	Pro	Phe
85					90					95					100
Lys	Pro	Ile	Thr	Arg	Lys	Ser	Val	Gly	His	Arg	Met	Gly	Gly	Gly	Lys
				105					110						115
Gly	Ala	Ile	Asp	His	Tyr	Val	Thr	Pro	Val	Lys	Ala	Gly	Arg	Leu	Val
			120					125					130		
Val	Glu	Met	Gly	Gly	Arg	Cys	Glu	Phe	Glu	Glu	Val	Gln	Gly	Phe	Leu
		135					140					145			
Asp	Gln	Val	Ala	His	Lys	Leu	Pro	Phe	Ala	Ala	Lys	Ala	Val	Ser	Arg
		150				155						160			
Gly	Thr	Leu	Glu	Lys	Met	Arg	Lys	Asp	Gln	Glu	Glu	Arg	Glu	Arg	Asn
165					170				175						180
Asn	Gln	Asn	Pro	Trp	Thr	Phe	Glu	Arg	Ile	Ala	Thr	Ala	Asn	Met	Leu
				185					190						195
Gly	Ile	Arg	Lys	Val	Leu	Ser	Pro	Tyr	Asp	Leu	Thr	His	Lys	Gly	Lys
			200					205					210		
Tyr	Trp	Gly	Lys	Phe	Tyr	Met	Pro	Lys	Arg	Val					
		215					220								

<210> 194
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -48..-1

<400> 194

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe	Ser
			-45					-40					-35		
Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Asp	Ile	Ile	Asn	Ser	Leu
		-30					-25					-20			
Val	Thr	Thr	Val	Phe	Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro
	-15				-10					-5					
Glu	Thr	Thr	Thr	Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr
1				5				10					15		
Ala	Val	Cys	Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu
		20					25						30		
Phe	Asn	Pro	Ser	Gly	Pro	Tyr	Gln	Lys	Lys	Pro	Val	His	Glu	Lys	Lys
		35					40					45			
Glu	Val	Leu													
		50													

<210> 195
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 195

Met	Ser	Asn	Thr	His	Thr	Val	Leu	Val	Ser	Leu	Pro	His	Pro	His	Pro
	-30					-25					-20				

Ala Leu Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro
 -15 -10 -5 1
 Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser
 5 10 15
 Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser
 20 25 30
 Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp
 35 40 45
 Leu
 50

<210> 196
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>

<400> 196

Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu Leu Thr
 1 5 10 15
 Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp His Gly
 20 25 30
 Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu Leu Glu Pro
 35 40 45
 Ser Lys Phe Ser Lys Gln Ala Glu Asn Glu Lys Lys Tyr Tyr Ile
 50 55 60
 Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu Ser Phe Phe
 65 70 75 80
 Gly Leu Glu Lys Leu Thr Asn Leu Gly Leu Gly Glu Arg Lys Val
 85 90 95
 Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val Ser His Leu
 100 105 110
 Gly Ile Leu Ala Val Gln Glu Gly Lys His Phe His Ser His Asn His
 115 120 125
 Gln His Ser His Asn His Leu Asn Ser Glu Asn Gln Thr Val Thr Ser
 130 135 140
 Val Ser Thr Lys Lys Lys
 145 150

<210> 197
 <211> 273
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
 <222> -45..-1

<400> 197

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
 -45 -40 -35 -30
 Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
 -25 -20 -15
 Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
 -10 -5 1

Lys	Asp	Phe	Asp	Cys	Asn	Thr	Arg	Gln	Pro	Gly	Cys	Ser	Asn	Val	Cys
5						10					15				
Phe	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln
20					25					30					35
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala
				40					45					50	
Tyr	Arg	Glu	Val	Gln	Glu	Lys	Arg	His	Arg	Glu	Ala	His	Gly	Glu	Asn
			55					60					65		
Ser	Gly	Arg	Leu	Tyr	Leu	Asn	Pro	Gly	Lys	Lys	Arg	Gly	Gly	Leu	Trp
	70					75					80				
Trp	Thr	Tyr	Val	Cys	Ser	Leu	Val	Phe	Lys	Ala	Ser	Val	Asp	Ile	Ala
	85					90					95				
Phe	Leu	Tyr	Val	Phe	His	Ser	Phe	Tyr	Pro	Lys	Tyr	Ile	Leu	Pro	Pro
100					105					110					115
Val	Val	Lys	Cys	His	Ala	Asp	Pro	Cys	Pro	Asn	Ile	Val	Asp	Cys	Phe
				120					125					130	
Ile	Ser	Lys	Pro	Ser	Glu	Lys	Asn	Ile	Phe	Thr	Leu	Phe	Met	Val	Ala
			135					140					145		
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Val	Glu	Leu	Ile	Tyr	Leu
	150						155					160			
Val	Ser	Lys	Arg	Cys	His	Glu	Cys	Leu	Ala	Ala	Arg	Lys	Ala	Gln	Ala
	165					170					175				
Met	Cys	Thr	Gly	His	His	Pro	His	Asp	Thr	Thr	Ser	Ser	Cys	Lys	Gln
180					185					190					195
Asp	Asp	Leu	Leu	Ser	Gly	Asp	Leu	Ile	Phe	Leu	Gly	Ser	Asp	Ser	His
				200					205					210	
Pro	Pro	Leu	Leu	Pro	Asp	Arg	Pro	Arg	Asp	His	Val	Lys	Lys	Thr	Ile
			215					220					225		
Leu															

<210> 198
 <211> 413
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37..-1

<400> 198

Met	Ala	Ser	Lys	Ile	Leu	Leu	Asn	Val	Gln	Glu	Glu	Val	Thr	Cys	Pro
	-35						-30					-25			
Ile	Cys	Leu	Glu	Leu	Leu	Thr	Glu	Pro	Leu	Ser	Leu	Asp	Cys	Gly	His
	-20					-15					-10				
Ser	Leu	Cys	Arg	Ala	Cys	Ile	Thr	Val	Ser	Asn	Lys	Glu	Ala	Val	Thr
-5					1				5					10	
Ser	Met	Gly	Gly	Lys	Ser	Ser	Cys	Pro	Val	Cys	Gly	Ile	Ser	Tyr	Ser
		15					20						25		
Phe	Glu	His	Leu	Gln	Ala	Asn	Gln	His	Leu	Ala	Asn	Ile	Val	Glu	Arg
	30						35					40			
Leu	Lys	Glu	Val	Lys	Leu	Ser	Pro	Asp	Asn	Gly	Lys	Lys	Arg	Asp	Leu
	45					50					55				
Cys	Asp	His	His	Gly	Glu	Lys	Leu	Leu	Leu	Phe	Cys	Lys	Glu	Asp	Arg
60					65					70					75
Lys	Val	Ile	Cys	Trp	Leu	Cys	Glu	Arg	Ser	Gln	Glu	His	Arg	Gly	His
			80						85					90	
His	Thr	Val	Leu	Thr	Glu	Glu	Val	Phe	Lys	Glu	Cys	Gln	Glu	Lys	Leu

			95					100					105				
Gln	Ala	Val	Leu	Lys	Arg	Leu	Lys	Lys	Glu	Glu	Glu	Glu	Ala	Glu	Lys		
		110						115					120				
Leu	Glu	Ala	Asp	Ile	Arg	Glu	Glu	Lys	Thr	Ser	Trp	Lys	Tyr	Gln	Val		
		125						130				135					
Gln	Thr	Glu	Arg	Gln	Arg	Ile	Gln	Thr	Glu	Phe	Asp	Gln	Leu	Arg	Ser		
140					145					150					155		
Ile	Leu	Asn	Asn	Glu	Gln	Arg	Glu	Leu	Gln	Arg	Leu	Glu	Glu	Glu			
			160					165				170					
Glu	Lys	Lys	Thr	Leu	Asp	Lys	Phe	Ala	Glu	Ala	Glu	Asp	Glu	Leu	Val		
		175						180				185					
Gln	Gln	Lys	Gln	Leu	Val	Arg	Glu	Leu	Ile	Ser	Asp	Val	Glu	Cys	Arg		
		190						195				200					
Ser	Gln	Trp	Ser	Thr	Met	Glu	Leu	Leu	Gln	Asp	Met	Ser	Gly	Ile	Met		
		205					210				215						
Lys	Trp	Ser	Glu	Ile	Trp	Arg	Leu	Lys	Lys	Pro	Lys	Met	Val	Ser	Lys		
220					225					230					235		
Lys	Leu	Lys	Thr	Val	Phe	His	Ala	Pro	Asp	Leu	Ser	Arg	Met	Leu	Gln		
				240					245					250			
Met	Phe	Arg	Glu	Leu	Thr	Ala	Val	Arg	Cys	Tyr	Trp	Val	Asp	Val	Thr		
			255					260				265					
Leu	Asn	Ser	Val	Asn	Leu	Asn	Leu	Asn	Leu	Val	Leu	Ser	Glu	Asp	Gln		
		270					275					280					
Arg	Gln	Val	Ile	Ser	Val	Pro	Ile	Trp	Pro	Phe	Gln	Cys	Tyr	Asn	Tyr		
		285					290				295						
Gly	Val	Leu	Gly	Ser	Gln	Tyr	Phe	Ser	Ser	Gly	Lys	His	Tyr	Trp	Glu		
300					305					310					315		
Val	Asp	Val	Ser	Lys	Thr	Ala	Trp	Ile	Leu	Gly	Val	Tyr	Cys	Arg			
				320					325					330			
Thr	Tyr	Ser	Arg	His	Met	Lys	Tyr	Val	Val	Arg	Arg	Cys	Ala	Asn	Arg		
			335					340				345					
Gln	Asn	Leu	Tyr	Thr	Lys	Tyr	Arg	Pro	Leu	Phe	Gly	Tyr	Trp	Val	Ile		
		350					355					360					
Gly	Leu	Gln	Asn	Lys	Cys	Lys	Tyr	Gly	Ala	Lys	Lys	Lys					
		365					370					375					

<210> 199

<211> 393

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19...-1

<400> 199

Met	Arg	Thr	Leu	Phe	Asn	Leu	Leu	Trp	Leu	Ala	Leu	Ala	Cys	Ser	Pro		
				-15					-10					-5			
Val	His	Thr	Thr	Leu	Ser	Lys	Ser	Asp	Ala	Lys	Lys	Ala	Ala	Ser	Lys		
			1				5					10					
Thr	Leu	Leu	Glu	Lys	Ser	Gln	Phe	Ser	Asp	Lys	Pro	Val	Gln	Asp	Arg		
			15			20					25						
Gly	Leu	Val	Val	Thr	Asp	Leu	Lys	Ala	Glu	Ser	Val	Val	Leu	Glu	His		
30					35					40					45		
Arg	Ser	Tyr	Cys	Ser	Ala	Lys	Ala	Arg	Asp	Arg	His	Phe	Ala	Gly	Asp		
				50					55					60			
Val	Leu	Gly	Tyr	Val	Thr	Pro	Trp	Asn	Ser	His	Gly	Tyr	Asp	Val	Thr		

		65					70					75			
Lys	Val	Phe	Gly	Ser	Lys	Phe	Thr	Gln	Ile	Ser	Pro	Val	Trp	Leu	Gln
	80						85					90			
Leu	Lys	Arg	Arg	Gly	Arg	Glu	Met	Phe	Glu	Val	Thr	Gly	Leu	His	Asp
	95					100					105				
Val	Asp	Gln	Gly	Trp	Met	Arg	Ala	Val	Arg	Lys	His	Ala	Lys	Gly	Leu
110					115					120					125
His	Ile	Val	Pro	Arg	Leu	Leu	Phe	Glu	Asp	Trp	Thr	Tyr	Asp	Asp	Phe
			130						135					140	
Arg	Asn	Val	Leu	Asp	Ser	Glu	Asp	Glu	Ile	Glu	Glu	Leu	Ser	Lys	Thr
		145						150					155		
Val	Val	Gln	Val	Ala	Lys	Asn	Gln	His	Phe	Asp	Gly	Phe	Val	Val	Glu
	160						165					170			
Val	Trp	Asn	Gln	Leu	Leu	Ser	Gln	Lys	Arg	Val	Gly	Leu	Ile	His	Met
	175					180					185				
Leu	Thr	His	Leu	Ala	Glu	Ala	Leu	His	Gln	Ala	Arg	Leu	Leu	Ala	Leu
190					195					200					205
Leu	Val	Ile	Pro	Pro	Ala	Ile	Thr	Pro	Gly	Thr	Asp	Gln	Leu	Gly	Met
			210						215					220	
Phe	Thr	His	Lys	Glu	Phe	Glu	Gln	Leu	Ala	Pro	Val	Leu	Asp	Gly	Phe
		225						230					235		
Ser	Leu	Met	Thr	Tyr	Asp	Tyr	Ser	Thr	Ala	His	Gln	Pro	Gly	Pro	Asn
	240						245					250			
Ala	Pro	Leu	Ser	Trp	Val	Arg	Ala	Cys	Val	Gln	Val	Leu	Asp	Pro	Lys
	255					260					265				
Ser	Lys	Trp	Arg	Ser	Lys	Ile	Leu	Leu	Gly	Leu	Asn	Phe	Tyr	Gly	Met
270					275					280					285
Asp	Tyr	Ala	Thr	Ser	Lys	Asp	Ala	Arg	Glu	Pro	Val	Val	Gly	Ala	Arg
			290						295					300	
Tyr	Ile	Gln	Thr	Leu	Lys	Asp	His	Arg	Pro	Arg	Met	Val	Trp	Asp	Ser
			305					310					315		
Gln	Ala	Ser	Glu	His	Phe	Phe	Glu	Tyr	Lys	Lys	Ser	Arg	Ser	Gly	Arg
	320						325					330			
His	Val	Val	Phe	Tyr	Pro	Thr	Leu	Lys	Ser	Leu	Gln	Val	Arg	Leu	Glu
	335					340					345				
Leu	Ala	Arg	Glu	Leu	Gly	Val	Gly	Val	Ser	Ile	Trp	Glu	Leu	Gly	Gln
350					355					360					365
Gly	Leu	Asp	Tyr	Phe	Tyr	Asp	Leu	Leu							
				370											

<210> 200
 <211> 381
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

<400> 200
 Met Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr
 -10 -5 1
 Thr Val Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Pro Leu Pro Val
 5 10 15
 Glu Ala Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe
 20 25 30 35
 Asp Asp Leu Pro Ala Arg Phe Gly Tyr Arg Leu Pro Ala Glu Gly Leu

				40					45					50			
Lys	Gly	Phe	Leu	Ile	Asn	Ser	Lys	Pro	Glu	Asn	Ala	Cys	Glu	Pro	Ile		
		55						60					65				
Val	Pro	Pro	Pro	Val	Lys	Asp	Asn	Ser	Ser	Gly	Thr	Phe	Ile	Val	Leu		
	70					75						80					
Ile	Arg	Arg	Leu	Asp	Cys	Asn	Phe	Asp	Ile	Lys	Val	Leu	Asn	Ala	Gln		
	85				90					95							
Arg	Ala	Gly	Tyr	Lys	Ala	Ala	Ile	Val	His	Asn	Val	Asp	Ser	Asp	Asp		
100					105				110						115		
Leu	Ile	Ser	Met	Gly	Ser	Asn	Asp	Ile	Glu	Val	Leu	Lys	Lys	Ile	Asp		
			120						125					130			
Ile	Pro	Ser	Val	Phe	Ile	Gly	Glu	Ser	Ser	Ala	Ser	Ser	Leu	Lys	Asp		
		135					140						145				
Glu	Phe	Thr	Tyr	Glu	Lys	Gly	Gly	His	Leu	Ile	Leu	Val	Pro	Glu	Phe		
	150					155						160					
Ser	Leu	Pro	Leu	Glu	Tyr	Tyr	Leu	Ile	Pro	Phe	Leu	Ile	Ile	Val	Gly		
	165				170					175							
Ile	Cys	Leu	Ile	Leu	Ile	Val	Ile	Phe	Met	Ile	Thr	Lys	Phe	Val	Gln		
180					185				190						195		
Asp	Arg	His	Arg	Ala	Arg	Arg	Asn	Arg	Leu	Arg	Lys	Asp	Gln	Leu	Lys		
			200						205					210			
Lys	Leu	Pro	Val	His	Lys	Phe	Lys	Lys	Gly	Asp	Glu	Tyr	Asp	Val	Cys		
		215					220						225				
Ala	Ile	Cys	Leu	Asp	Glu	Tyr	Glu	Asp	Gly	Asp	Lys	Leu	Arg	Ile	Leu		
	230						235					240					
Pro	Cys	Ser	His	Ala	Tyr	His	Cys	Lys	Cys	Val	Asp	Pro	Trp	Leu	Thr		
	245					250					255						
Lys	Thr	Lys	Lys	Thr	Cys	Pro	Val	Cys	Arg	Gln	Lys	Val	Val	Pro	Ser		
260					265					270					275		
Gln	Gly	Asp	Ser	Asp	Ser	Asp	Thr	Asp	Ser	Ser	Gln	Glu	Glu	Asn	Glu		
			280					285						290			
Val	Thr	Glu	His	Thr	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Ser	Val	Ser	Ala		
		295					300						305				
Gln	Ser	Phe	Gly	Ala	Leu	Ser	Glu	Ser	Arg	Ser	His	Gln	Asn	Met	Thr		
	310						315					320					
Glu	Ser	Ser	Asp	Tyr	Glu	Glu	Asp	Asp	Asn	Glu	Asp	Thr	Asp	Ser	Ser		
	325					330					335						
Asp	Ala	Glu	Asn	Glu	Ile	Asn	Glu	His	Asp	Val	Val	Val	Gln	Leu	Gln		
340					345				350						355		
Pro	Asn	Gly	Glu	Arg	Asp	Tyr	Asn	Ile	Ala	Asn	Thr	Val					
			360						365								

<210> 201
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 201
 Met Asp Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe
 -40 -35 -30
 Val Gly Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe
 -25 -20 -15
 Ser Leu Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp

-10					-5					1				5	
Met	Cys	Leu	Lys	Ile	Ile	Arg	Glu	Tyr	Glu	Arg	Ala	Val	Val	Phe	Arg
			10					15					20		
Leu	Gly	Arg	Ile	Gln	Ala	Asp	Lys	Ala	Lys	Gly	Pro	Gly	Leu	Ile	Leu
		25					30					35			
Val	Leu	Pro	Cys	Ile	Asp	Val	Phe	Val	Lys	Val	Asp	Leu	Arg	Thr	Val
	40					45					50				
Thr	Cys	Asn	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Arg	Asp	Ser	Val	Thr
55					60					65				70	
Thr	Gln	Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Ile	Tyr	Ser	Ala	Val	Ser
			75					80					85		
Ala	Val	Ala	Asn	Val	Asn	Asp	Val	His	Gln	Ala	Thr	Phe	Leu	Leu	Ala
			90					95					100		
Gln	Thr	Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Gln	Thr	Leu	Ser	Gln	Ile
		105					110					115			
Leu	Ala	Gly	Arg	Glu	Glu	Ile	Ala	His	Ser	Ile	Gln	Thr	Leu	Leu	Asp
	120					125					130				
Asp	Ala	Thr	Glu	Leu	Trp	Gly	Ile	Arg	Val	Ala	Arg	Val	Glu	Ile	Lys
135					140				145					150	
Asp	Val	Arg	Ile	Pro	Val	Gln	Leu	Gln	Arg	Ser	Met	Ala	Ala	Glu	Ala
				155				160					165		
Glu	Ala	Thr	Arg	Glu	Ala	Arg	Ala	Lys	Val	Leu	Ala	Ala	Glu	Gly	Glu
			170					175					180		
Met	Ser	Ala	Ser	Lys	Ser	Leu	Lys	Ser	Ala	Ser	Met	Val	Leu	Ala	Glu
		185					190					195			
Ser	Pro	Ile	Ala	Leu	Gln	Leu	Arg	Tyr	Leu	Gln	Thr	Leu	Ser	Thr	Val
	200					205					210				
Ala	Thr	Glu	Lys	Asn	Ser	Thr	Ile	Val	Phe	Pro	Leu	Pro	Met	Asn	Ile
215					220				225					230	
Leu	Glu	Gly	Ile	Gly	Gly	Val	Ser	Tyr	Asp	Asn	His	Lys	Lys	Leu	Pro
			235					240					245		

Asn Lys Ala

<210> 202

<211> 92

<212> PRT

<213> Homo sapiens

<220>

<400> 202

Met	Pro	Pro	Arg	Asn	Leu	Leu	Glu	Leu	Leu	Ile	Asn	Ile	Lys	Ala	Gly
1				5				10					15		
Thr	Tyr	Leu	Pro	Gln	Ser	Tyr	Leu	Ile	His	Glu	His	Met	Val	Ile	Thr
			20				25					30			
Asp	Arg	Ile	Glu	Asn	Ile	Asp	His	Leu	Gly	Phe	Phe	Ile	Tyr	Arg	Leu
		35				40					45				
Cys	His	Asp	Lys	Glu	Thr	Tyr	Lys	Leu	Gln	Arg	Arg	Glu	Thr	Ile	Lys
	50					55				60					
Gly	Ile	Gln	Lys	Arg	Glu	Ala	Ser	Asn	Cys	Phe	Ala	Ile	Arg	His	Phe
65					70				75					80	
Glu	Asn	Lys	Phe	Ala	Val	Glu	Thr	Leu	Ile	Cys	Ser				
				85				90							

<210> 203

<211> 127

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -63..-1

<400> 203

Met	Ser	Ala	Ala	Gly	Ala	Arg	Gly	Leu	Arg	Ala	Thr	Tyr	His	Arg	Leu
			-60					-55					-50		
Pro	Asp	Lys	Val	Glu	Leu	Met	Leu	Pro	Glu	Lys	Leu	Arg	Pro	Leu	Tyr
		-45					-40					-35			
Asn	His	Pro	Ala	Gly	Pro	Arg	Thr	Val	Phe	Phe	Trp	Ala	Pro	Ile	Met
	-30					-25					-20				
Lys	Trp	Gly	Leu	Val	Cys	Ala	Gly	Leu	Ala	Asp	Met	Ala	Arg	Pro	Ala
-15					-10					-5					1
Glu	Lys	Leu	Ser	Thr	Ala	Gln	Ser	Ala	Val	Leu	Met	Ala	Thr	Gly	Phe
			5					10						15	
Ile	Trp	Ser	Arg	Tyr	Ser	Leu	Val	Ile	Ile	Pro	Lys	Asn	Trp	Ser	Leu
		20					25					30			
Phe	Ala	Val	Asn	Phe	Phe	Val	Gly	Ala	Ala	Gly	Ala	Ser	Gln	Leu	Phe
	35					40				45					
Arg	Ile	Trp	Arg	Tyr	Asn	Gln	Glu	Leu	Lys	Ala	Lys	Ala	His	Lys	
50					55					60					

<210> 204
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 204

Met	Lys	Gly	Trp	Gly	Trp	Leu	Ala	Leu	Leu	Leu	Gly	Ala	Leu	Leu	Gly
-20					-15					-10					-5
Thr	Ala	Trp	Ala	Arg	Arg	Ser	Gln	Asp	Leu	His	Cys	Gly	Ala	Cys	Arg
			1				5					10			
Ala	Leu	Val	Asp	Glu	Leu	Glu	Trp	Glu	Ile	Ala	Gln	Val	Asp	Pro	Lys
		15					20				25				
Lys	Thr	Ile	Gln	Met	Gly	Ser	Phe	Arg	Ile	Asn	Pro	Asp	Gly	Ser	Gln
	30					35				40					
Ser	Val	Val	Glu	Val	Thr	Val	Thr	Val	Pro	Pro	Asn	Lys	Val	Ala	His
45					50					55					60
Ser	Gly	Phe	Gly												

<210> 205
<211> 182
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 205

Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
-20 -15 -10 -5
Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg
1 5 10
Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
15 20 25
Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln
30 35 40
Ser Val Val Glu Val Pro Tyr Ala Arg Ser Glu Ala His Leu Thr Glu
45 50 55 60
Leu Leu Glu Glu Ile Cys Asp Arg Met Lys Glu Tyr Gly Glu Gln Ile
65 70 75
Asp Pro Ser Thr His Arg Lys Asn Tyr Val Arg Val Val Gly Arg Asn
80 85 90
Gly Glu Ser Ser Glu Leu Asp Leu Gln Gly Ile Arg Ile Asp Ser Asp
95 100 105
Ile Ser Gly Thr Leu Lys Phe Ala Cys Gly Ser Ile Val Glu Glu Tyr
110 115 120
Glu Asp Glu Leu Ile Glu Phe Phe Ser Arg Glu Ala Asp Asn Val Lys
125 130 135 140
Asp Lys Leu Cys Ser Lys Arg Thr Asp Leu Cys Asp His Ala Leu His
145 150 155
Ile Ser His Asp Glu Leu
160

<210> 206

<211> 71

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25..-1

<400> 206

Met Pro Ala Gly Val Pro Met Ser Thr Tyr Leu Lys Met Phe Ala Ala
-25 -20 -15 -10
Ser Leu Leu Ala Met Cys Ala Gly Ala Glu Val Val His Arg Tyr Tyr
-5 1 5
Arg Pro Asp Leu Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu
10 15 20
Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro Gln Val
25 30 35
Ser Gln Gln Glu Glu Leu Lys
40 45

<210> 207

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<400> 207

Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe Leu

<400> 205

Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
-20 -15 -10 -5
Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg
1 5 10
Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
15 20 25
Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln
30 35 40
Ser Val Val Glu Val Pro Tyr Ala Arg Ser Glu Ala His Leu Thr Glu
45 50 55 60
Leu Leu Glu Glu Ile Cys Asp Arg Met Lys Glu Tyr Gly Glu Gln Ile
65 70 75
Asp Pro Ser Thr His Arg Lys Asn Tyr Val Arg Val Val Gly Arg Asn
80 85 90
Gly Glu Ser Ser Glu Leu Asp Leu Gln Gly Ile Arg Ile Asp Ser Asp
95 100 105
Ile Ser Gly Thr Leu Lys Phe Ala Cys Gly Ser Ile Val Glu Glu Tyr
110 115 120
Glu Asp Glu Leu Ile Glu Phe Phe Ser Arg Glu Ala Asp Asn Val Lys
125 130 135 140
Asp Lys Leu Cys Ser Lys Arg Thr Asp Leu Cys Asp His Ala Leu His
145 150 155
Ile Ser His Asp Glu Leu
160

<210> 206

<211> 71

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25..-1

<400> 206

Met Pro Ala Gly Val Pro Met Ser Thr Tyr Leu Lys Met Phe Ala Ala
-25 -20 -15 -10
Ser Leu Leu Ala Met Cys Ala Gly Ala Glu Val Val His Arg Tyr Tyr
-5 1 5
Arg Pro Asp Leu Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu
10 15 20
Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro Gln Val
25 30 35
Ser Gln Gln Glu Glu Leu Lys
40 45

<210> 207

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<400> 207

Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe Leu

1		5		10		15									
Cys	Thr	Asp	Arg	Asp	Cys	Asn	Val	Ile	Leu	Gly	Ser	Ala	Gln	Glu	Phe
		20						25					30		
Leu	Lys	Pro	Ser	Asp	Ser	Phe	Ser	Ala	Gly	Glu	Pro	Arg	Val	Leu	Gly
		35					40					45			
Leu	Ala	Met	Val	Pro	Gly	His	His	Ile	Val	Ser	Ile	Glu	Val	Gln	Arg
	50					55					60				
Glu	Ser	Leu	Thr	Gly	Pro	Pro	Tyr	Leu							
65					70										

<210> 208
 <211> 169
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -150..-1

<400> 208

Met	Ala	Glu	Thr	Lys	Asp	Thr	Ala	Gln	Met	Leu	Val	Thr	Phe	Lys	Asp
-150					-145					-140					-135
Val	Ala	Val	Thr	Phe	Thr	Arg	Glu	Glu	Trp	Arg	Gln	Leu	Asp	Leu	Ala
				-130					-125						-120
Gln	Arg	Thr	Leu	Tyr	Arg	Glu	Gly	Ile	Gly	Phe	Pro	Lys	Pro	Glu	Leu
				-115				-110					-105		
Val	His	Leu	Leu	Glu	His	Gly	Gln	Glu	Leu	Trp	Ile	Val	Lys	Arg	Gly
				-100			-95					-90			
Leu	Ser	His	Ala	Thr	Cys	Ala	Glu	Phe	His	Ser	Cys	Cys	Pro	Gly	Trp
	-85					-80					-75				
Ser	Ala	Val	Xaa	Arg	His	Leu	Ser	Ser	Leu	Gln	Leu	Leu	Pro	Pro	Glu
	-70				-65					-60					-55
Phe	Lys	Gly	Phe	Ser	Cys	Leu	Ser	Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Arg
				-50					-45					-40	
Arg	Pro	Pro	Pro	Cys	Pro	Ala	Gly	Phe	Phe	Val	Phe	Leu	Val	Glu	Thr
				-35				-30					-25		
Gly	Leu	His	His	Val	Gly	Gln	Ala	Gly	Leu	Glu	Leu	Leu	Thr	Ser	Cys
		-20				-15						-10			
Ser	Pro	Pro	Ala	Ser	Ala	Ser	Gln	Ser	Ala	Ala	Ile	Thr	Gly	Val	Ser
	-5				1				5						10
His	Arg	Ala	Arg	Gln	Arg	Lys	Thr	Ala							
				15											

<210> 209
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 209

Met	Glu	Leu	Ile	Ser	Pro	Thr	Val	Ile	Ile	Ile	Leu	Gly	Cys	Leu	Ala
		-20					-15					-10			
Leu	Phe	Leu	Leu	Leu	Gln	Arg	Lys	Asn	Leu	Arg	Arg	Pro	Pro	Cys	Ile

-5		1		5		10
Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala						
	15		20		25	
Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Val Cys Gly Arg Gly						
	30	35	40			
Arg Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu Phe						
	45	50				

<210> 210
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54..-1

<400> 210
Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys Asp
Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala
Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu Leu
Val Ser Leu Val Glu Ser Ile Trp Leu His Ile Thr Glu Asn Gln Ile
Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu Lys
Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln

<210> 211
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -22..-1

<400> 211
Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala
Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Tyr Gly Pro Ile Phe
Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe Val Thr Glu Glu Glu
Gly Ile Asn Val Phe Leu Lys Ser Lys Lys Lys Lys

<210> 212

<211> 89
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -16..-1

<400> 212
 Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
 -15 -10 -5
 Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
 1 5 10 15
 Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
 20 25 30
 Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile
 35 40 45
 Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp Trp Ala
 50 55 60
 Glu Ala Gly Ala Ser Leu Tyr Ser Pro
 65 70

<210> 213
 <211> 109
 <212> PRT
 <213> Homo sapiens

<220>

<400> 213
 Met Lys Val Asp Lys Asp Arg Gln Met Val Val Leu Glu Glu Glu Phe
 1 5 10 15
 Arg Asn Ile Ser Pro Glu Glu Leu Lys Met Glu Leu Pro Glu Arg Gln
 20 25 30
 Pro Arg Phe Val Val Tyr Ser Tyr Lys Tyr Val Arg Asp Asp Gly Arg
 35 40 45
 Val Ser Tyr Pro Leu Cys Phe Ile Phe Ser Ser Pro Val Gly Cys Lys
 50 55 60
 Pro Glu Gln Gln Met Met Tyr Ala Gly Ser Lys Asn Arg Leu Val Gln
 65 70 75 80
 Thr Ala Glu Leu Thr Lys Val Phe Glu Ile Arg Thr Thr Asp Asp Leu
 85 90 95
 Thr Glu Ala Trp Leu Gln Glu Lys Leu Ser Phe Phe Arg
 100 105

<210> 214
 <211> 114
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -103..-1

<400> 214
 Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile

			-100					-95				-90			
Lys	Lys	Lys	Gln	Gln	Asp	Val	Leu	Gly	Phe	Leu	Glu	Ala	Asn	Lys	Ile
		-85					-80					-75			
Gly	Phe	Glu	Glu	Lys	Asp	Ile	Ala	Ala	Asn	Glu	Glu	Asn	Arg	Lys	Trp
	-70				-65						-60				
Met	Arg	Glu	Asn	Val	Pro	Glu	Asn	Ser	Arg	Pro	Ala	Thr	Gly	Asn	Pro
-55					-50				-45						-40
Leu	Pro	Pro	Gln	Ile	Phe	Asn	Glu	Ser	Gln	Tyr	Arg	Gly	Asp	Tyr	Asp
			-35						-30					-25	
Ala	Phe	Phe	Glu	Ala	Arg	Glu	Asn	Asn	Ala	Val	Tyr	Ala	Phe	Leu	Gly
		-20					-15					-10			
Leu	Thr	Ala	Pro	Ser	Gly	Ser	Lys	Glu	Ala	Glu	Val	Gln	Ala	Lys	Gln
		-5					1				5				
Gln	Ala														
10															

<210> 215
 <211> 124
 <212> PRT
 <213> Homo sapiens

<220>															
<221> SIGNAL															
<222> -97..-1															
<400> 215															
Met	Ala	Asp	Asp	Leu	Lys	Arg	Phe	Leu	Tyr	Lys	Lys	Leu	Pro	Ser	Val
		-95					-90					-85			
Glu	Gly	Leu	His	Ala	Ile	Val	Val	Ser	Asp	Arg	Asp	Gly	Val	Pro	Val
	-80					-75					-70				
Ile	Lys	Val	Ala	Asn	Asp	Asn	Ala	Pro	Glu	His	Ala	Leu	Arg	Pro	Gly
-65					-60					-55					-50
Phe	Leu	Ser	Thr	Phe	Ala	Leu	Ala	Thr	Asp	Gln	Gly	Ser	Lys	Leu	Gly
			-45						-40					-35	
Leu	Ser	Lys	Asn	Lys	Ser	Ile	Ile	Cys	Tyr	Tyr	Asn	Thr	Tyr	Gln	Val
			-30					-25						-20	
Val	Gln	Phe	Asn	Arg	Leu	Pro	Leu	Val	Val	Ser	Phe	Ile	Ala	Ser	Ser
		-15					-10					-5			
Ser	Ala	Asn	Thr	Gly	Leu	Ile	Val	Ser	Leu	Glu	Lys	Glu	Leu	Ala	Pro
	1				5					10					15
Leu	Phe	Glu	Glu	Leu	Arg	Gln	Val	Val	Glu	Val	Ser				
			20					25							

<210> 216
 <211> 93
 <212> PRT
 <213> Homo sapiens

<220>															
<221> SIGNAL															
<222> -22..-1															
<400> 216															
Met	Lys	Pro	Val	Leu	Pro	Leu	Gln	Phe	Leu	Val	Val	Phe	Cys	Leu	Ala
	-20						-15					-10			
Leu	Gln	Leu	Val	Pro	Gly	Ser	Pro	Lys	Gln	Arg	Val	Leu	Lys	Tyr	Ile

-5						1				5					10
Leu	Glu	Pro	Pro	Pro	Cys	Ile	Ser	Ala	Pro	Glu	Asn	Cys	Thr	His	Leu
				15					20					25	
Cys	Thr	Met	Gln	Glu	Asp	Cys	Glu	Lys	Gly	Phe	Gln	Cys	Cys	Ser	Ser
			30					35					40		
Phe	Cys	Gly	Ile	Val	Cys	Ser	Ser	Glu	Thr	Phe	Gln	Lys	Arg	Asn	Arg
		45					50					55			
Ile	Lys	His	Lys	Gly	Ser	Glu	Val	Ile	Met	Pro	Ala	Asn			
	60					65					70				

<210> 217
 <211> 207
 <212> PRT
 <213> Homo sapiens

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 <221> SIGNAL
 <222> -42..-1

<400> 217

Met	His	Ile	Leu	Gln	Leu	Leu	Thr	Thr	Val	Asp	Asp	Gly	Ile	Gln	Ala
		-40					-35					-30			
Ile	Val	His	Cys	Pro	Asp	Thr	Gly	Lys	Asp	Ile	Trp	Asn	Leu	Leu	Phe
	-25					-20				-15					
Asp	Leu	Val	Cys	His	Glu	Phe	Cys	Gln	Ser	Asp	Asp	Pro	Pro	Ile	Ile
	-10				-5					1				5	
Leu	Gln	Glu	Gln	Lys	Thr	Val	Leu	Ala	Ser	Val	Phe	Ser	Val	Leu	Ser
			10					15					20		
Ala	Ile	Tyr	Ala	Ser	Gln	Thr	Glu	Gln	Glu	Tyr	Leu	Lys	Ile	Glu	Lys
		25					30					35			
Val	Asp	Leu	Pro	Leu	Ile	Asp	Ser	Leu	Ile	Arg	Val	Leu	Gln	Asn	Met
	40					45					50				
Glu	Gln	Cys	Gln	Lys	Lys	Pro	Glu	Asn	Ser	Ala	Glu	Ser	Asn	Thr	Glu
	55				60					65					70
Glu	Thr	Lys	Arg	Thr	Asp	Leu	Thr	Gln	Asp	Asp	Phe	His	Leu	Lys	Ile
			75					80					85		
Leu	Lys	Asp	Ile	Leu	Cys	Glu	Phe	Leu	Ser	Asn	Ile	Phe	Gln	Ala	Leu
		90					95						100		
Thr	Lys	Glu	Thr	Val	Ala	Gln	Gly	Val	Lys	Glu	Gly	Gln	Leu	Ser	Lys
	105						110					115			
Gln	Lys	Cys	Ser	Ser	Ala	Phe	Gln	Asn	Leu	Leu	Pro	Phe	Tyr	Ser	Pro
	120					125					130				
Val	Val	Glu	Asp	Phe	Ile	Lys	Ile	Leu	Arg	Glu	Val	Asp	Lys	Ala	Leu
	135				140					145					150
Ala	Asp	Asp	Leu	Glu	Lys	Asn	Phe	Pro	Ser	Leu	Lys	Val	Gln	Thr	
			155						160					165	

<210> 218
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>

<400> 218

Met Pro His Ser Lys Pro Leu Asp Trp Gly Leu Ser Ser Val Ala Glu

1		5		10		15									
Cys	Pro	Ala	Glu	Leu	Phe	Pro	Ser	Thr	Gly	Gly	Leu	Ala	Gly	Lys	Gly
		20						25					30		
Pro	Gly	Leu	Asp	Ile	Leu	Arg	Cys	Val	Leu	Ser	Pro	Trp	Ala	Ser	His
		35					40					45			
Phe	Pro	Ser	Leu	Ser	Leu	Gly	Val	Phe	Asn	Leu					
	50					55									

<210> 219
 <211> 56
 <212> PRT
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 <222> -27..-1

<400> 219
Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile Cys Leu
-25 -20 -15
Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg
-10 -5 1 5
Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val Arg Ala
10 15 20
Trp Cys Ile Gln Pro Trp Ala Lys
25

<210> 220
 <211> 162
 <212> PRT
 <213> Homo sapiens

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 <222> -94..-1

<400> 220
Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
-90 -85 -80
Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
-75 -70 -65
Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala
-60 -55 -50
Val Leu Phe Asn Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe
-45 -40 -35
Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly
-30 -25 -20 -15
Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His
-10 -5 1
Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp
5 10 15
Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val
20 25 30
Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro
35 40 45 50
His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val

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Arg Arg

<210> 221

<211> 154

<212> PRT

<213> Homo sapiens

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<221> SIGNAL

<222> -68..-1

<400> 221

Met	Ala	Ser	Ala	Ser	Ala	Arg	Gly	Asn	Gln	Asp	Lys	Asp	Ala	His	Phe
			-65					-60					-55		
Pro	Pro	Pro	Ser	Lys	Gln	Ser	Leu	Phe	Cys	Pro	Lys	Ser	Lys	Leu	
			-50				-45					-40			
His	Ile	His	Arg	Ala	Glu	Ile	Ser	Lys	Ile	Met	Arg	Glu	Cys	Gln	Glu
	-35					-30				-25					
Glu	Ser	Phe	Trp	Lys	Arg	Ala	Leu	Pro	Phe	Ser	Leu	Val	Ser	Met	Leu
	-20				-15				-10					-5	
Val	Thr	Gln	Gly	Leu	Val	Tyr	Gln	Gly	Tyr	Leu	Ala	Ala	Asn	Ser	Arg
				1				5					10		
Phe	Gly	Ser	Leu	Pro	Lys	Val	Ala	Leu	Ala	Gly	Leu	Leu	Gly	Phe	Gly
		15					20					25			
Leu	Gly	Lys	Val	Ser	Tyr	Ile	Gly	Val	Cys	Gln	Ser	Lys	Phe	His	Phe
	30					35				40					
Phe	Glu	Asp	Gln	Leu	Arg	Gly	Ala	Gly	Phe	Gly	Pro	Gln	His	Asn	Arg
	45				50				55					60	
His	Cys	Leu	Leu	Thr	Cys	Glu	Glu	Cys	Lys	Ile	Lys	His	Gly	Leu	Ser
				65					70					75	
Glu	Lys	Gly	Asp	Ser	Gln	Pro	Ser	Ala	Ser						
			80					85							

<210> 222

<211> 99

<212> PRT

<213> Homo sapiens

<220>

<400> 222

Met	Lys	Val	Glu	Glu	Glu	His	Thr	Asn	Ala	Ile	Gly	Thr	Leu	His	Gly
1			5						10					15	
Gly	Leu	Thr	Ala	Thr	Leu	Val	Asp	Asn	Ile	Ser	Thr	Met	Ala	Leu	Leu
			20					25					30		
Cys	Thr	Glu	Arg	Gly	Ala	Pro	Gly	Val	Ser	Val	Asp	Met	Asn	Ile	Thr
		35					40					45			
Tyr	Met	Ser	Pro	Ala	Lys	Leu	Gly	Glu	Asp	Ile	Val	Ile	Thr	Ala	His
	50					55					60				
Val	Leu	Lys	Gln	Gly	Lys	Thr	Leu	Ala	Phe	Thr	Ser	Val	Gly	Leu	Thr
	65				70					75				80	
Asn	Lys	Ala	Thr	Gly	Lys	Leu	Ile	Ala	Gln	Gly	Arg	His	Thr	Lys	His
				85					90					95	

Leu Gly Asn

<210> 223
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 <213> Homo sapiens

<220>
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 <222> -24..-1

<400> 223
 Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 -20 -15 -10
 Leu Ile Phe Leu Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser
 -5 1 5
 Pro Tyr Phe Lys Met His Lys Pro Val Thr Met
 10 15

<210> 224
 <211> 69
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -21..-1

<400> 224
 Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
 -20 -15 -10
 Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
 -5 1 5 10
 Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
 15 20 25
 Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
 30 35 40
 Val Leu Cys Gln Lys
 45

<210> 225
 <211> 78
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -18..-1

<400> 225
 Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser
 -15 -10 -5
 Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val
 1 5 10
 Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr
 15 20 25 30
 Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val

35 40 45
 Val Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala
 50 55 60

<210> 226
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47..-1

<400> 226
 Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser Thr Ala
 -45 -40 -35
 Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe Ser Ser
 -30 -25 -20
 Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe Cys Phe
 -15 -10 -5 1
 Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr Phe Pro
 5 10 15
 Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly Arg Phe
 20 25 30

<210> 227
 <211> 241
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -103..-1

<400> 227
 Met Trp Leu Asp Pro Val Phe Pro Leu Phe Pro Val Gly Asp His Tyr
 -100 -95 -90
 Leu Pro His Leu His Met Asp Val Leu Glu Gly Leu Ile Leu Val Leu
 -85 -80 -75
 Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu Arg Thr Val Thr Cys
 -70 -65 -60
 Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp Ser Val Thr Thr Gln
 -55 -50 -45 -40
 Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser Ala Val Ser Ala Val
 -35 -30 -25
 Ala Asn Val Asn Asp Val His Gln Ala Thr Phe Leu Leu Ala Gln Thr
 -20 -15 -10
 Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu Ser Gln Ile Leu Ala
 -5 1 5
 Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr Leu Leu Asp Asp Ala
 10 15 20 25
 Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val Glu Ile Lys Asp Val
 30 35 40
 Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala Glu Ala
 45 50 55
 Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu Met Asn

		60					65					70					
Ala	Ser	Lys	Ser	Leu	Lys	Ser	Ala	Ser	Met	Val	Leu	Ala	Glu	Ser	Pro		
	75					80					85						
Ile	Ala	Leu	Gln	Leu	Arg	Tyr	Leu	Gln	Thr	Leu	Ser	Thr	Val	Ala	Thr		
90					95					100					105		
Glu	Lys	Asn	Ser	Thr	Ile	Val	Phe	Pro	Leu	Pro	Met	Asn	Ile	Leu	Glu		
				110					115					120			
Gly	Ile	Gly	Gly	Val	Ser	Tyr	Asp	Asn	His	Lys	Lys	Leu	Pro	Asn	Lys		
			125					130					135				
Ala																	

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